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Gaps
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                                            Sequence 8, Application US/09102420B
Patent No. 6084155
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Johnson, Marie
APPLICANT: Ward, Eric
APPLICANT: Ward, Eric
APPLICANT: Ward, Eric
APPLICANT: Ward, Eric
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
TITLE OF INVENTION: OXIDASE ("PROTOX")
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,420B
FILING DATE: 22-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.4%; Score 99.5; DB 3; Best Local Similarity 20.1%; Pred. No. 0.13; Matches 82; Conservative 47; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: NO. 6084155artis Corporation
F: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38.241
REFERENCE/DOCKET NUMBER: CGC 1847/CIP3
TELECOMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/059,164
FILING DATE: 13-APR-1998
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
PRIOR APPLICATION DATA: 30-MAR-1998
PRIOR APPLICATION UNMBER: US 60/126,430
FILING DATE: 11-MAR-1998
PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA: APPLICATION UNMBER: US 66/012,705
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA: 28-FEB-1996
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FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-UN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 98/472,028
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 544 amino acids
amino acid
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Flore
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                                    JS-09-102-420B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQR----TMDRNEQTAWKAY--YPTLFE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 A-----ILSKIAARGD-------PVKTRHDSSGKRRNRRVSFSFHGGMOSLIN 284
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3.4%; Score 99.5; DB 3; Length 544;
Best Local Similarity 20.1%; Pred No. 0.13;
Matches 82; Conservative 47; Mismatches 115; Indels 163;
Matches Applied A
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                                                                         COMPUTER: 27709

COMPUTER: EBAPBLE FORM;
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DSS/MS-DDS
OPERATING SYSTEM: PC-DSS/MS-DDS
CURRENT MARSE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,603A
CLASSIPTCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION NUMBER: US 60/013,612
FILING DATE: 210-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 210-10-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 210-10-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 210-10-1996
ATTORNEY AGENT INFORMATION:
NAME: Melgs, J. Timothy
REFERENCE/DOCKET NUMBER: CGC 1847
TELEPHONE: (919) 541-8897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8897
TELEPHONE: (919) 541-8897
TELEPHONE: CHARRCTERISTICS:
TRUCKER CHARRCTERISTICS:
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TYPE: amino acid
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STATE: N
COUNTRY:
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19 IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78

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155 STKSKIALFFEPFLYKKANTRNSGKVSEEHLSESVGSFCERHFGREVVD--YFVD--PPV 210
                                                                                                                                                                                                                              130 VKTSAGHVATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDFDAEGQRVAVIG 189
                                                                                                                                                                                                                                                                                                           190 AGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQR----TMDRNEQTAWKAY--YPTLFE 243
                                                                                               95 DEGANTMTEGEWEASRLIDDLGLQDKQOYPNSQHKRYIVKDGAPALIPSDPISLMKSSVL 154
                                                                                                                                                   -------HHCDKIRGLRKDVYFGAEVVDARYARDLGTWT 129
                                                                                                                                                                                                                                                                                                                                                       244 A-----ILSKLAAKGD------PVKTRHDSSGKRRNRRVSFSFHGGMQSLIN 284
                                                                                                                                                                                                                                                                                                                                                                                               244 ASRKS-----RIGFPVQA----- PSVGIFEVSPEQREAYFEELWERGAFNFL---- 285
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09071296
Patent No. 617245
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
APPLICANT: Wolrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
                         94
                                                               KDWT-----WSC-------RYPDQKELLSYV-----------97
50 VVGAGVSGLAAAYRLRQSGVNVTVFEAADRAGG------KIRTNSEGGF------VW
                                                                                                                                                                                                                                                                   211 AGTSAGD------PESLSIRHAFPALWNLERKYGSVI-------VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 -ACQYREVMVDKKANRLVYDFWAKK---TRSRIVNPAKR-DLMAPLE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 PLSNVRRMKFTKGGAPVVLDFLPRMDYLPLSLMVTAFKKDDVKKPLE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/071,296
FILING DATE: 06-JUN-1995
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APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Socht
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Clba-Gelgy Corporation STREFT: 7 Skyline Drive CITY: Hawthorne STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 544 amino acids
amino acid
GY: linear
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MOLECULE TYPE: protein
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US-09-071-296-8
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                               Gaps
                                                                                                                                               : : 11: : DEGANTWIEGEWEASRLIDDIGLØDKQQYPNSQHKRYIVKDGAPALIPSDPISLMKSSVL 154
                                                                                                                                                                                                                                                    130 VKTSAGHVATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDFDAEGQRVAVIG 189
                                                                                                                                                                                                                                                                                                                  AGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQR----TMDRNEQTAWKAY--YPTLFE 243
                                                                                                                                                                                                                                                                                                                                                                                                   19 IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78
                                                                                                                          79 KDWT------WSC------RYPDQKELLSYV------WSC
                                                                                                                                                                                                                                                                                    211 AGTSAGD ----- PESLSIRHAFPALWNLERKYGSVI-----VG
                               Indels 163;
3.4%; Score 99.5; DB 4; Length 544;
20.1%; Pred. No. 0.13;
Live 47; Mismatches 115; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                              286 -ACQYREVMVDKKANRLVYDFWAKK---TRSRIVNPAKR-DLMAPLE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLSNVRRMKFTKGGAPVVLDFLPKMDYLPLSLMVTAFKKDDVKKPLE 391
                              Conservative
              Similarity
Query Match
Best Local Simi
Matches 82;
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Search completed: April 27, 2002, 07:46:43 Job time: 6700 sec

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April 26, 2002, 20:51:07; Search time 96.68 Seconds (without alignments) 3112.349 Million cell updates/sec
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206, App
20, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pending_Patents_NA_New:*

.: /cgn2_6/ptodata/1/pna_VUS06_NEW_COMB.seq:*

.: /cgn2_6/ptodata/1/pna_VUS06_NEW_COMB.seq:*

.: /cgn2_6/ptodata/1/pna_VUS08_NEW_COMB.seq:*

.: /cgn2_6/ptodata/1/pna_VUS08_NEW_COMB.seq:*

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.: /cgn2_6/ptodata/1/pna_VUS08_NEW_COMB.seq:*

.: /cgn2_6/ptodata/1/pna_VUS06_NEW_COMB.seq:*
                     Compugen Ltd
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US-09-975-254-11803

US-09-975-254-11803

US-09-540-210B-7546

US-09-540-209B-284

US-09-974-702-1

US-09-975-254-25703

US-10-107-431-27

US-10-107-431-27

US-10-107-431-27

US-10-107-431-27

US-10-107-431-27

US-10-107-20921-464

US-10-107-20921-464

US-09-975-254-29303

US-10-105-299-6550

US-09-980-771A-6

US-09-980-771A-6

US-09-980-771A-6

US-09-980-771A-7

US-09-980-771A-1

US-10-103-299-11932

US-10-103-299-11932

US-10-103-299-1181
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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RESULT 1
US-09-975-254-7839
is Sequence 7839, Application US/09975254
js General INFORMATION:
is APPLICANT: Byrum, Joseph R.
js APPLICANT: Byrum, Joseph R.
js APPLICANT: Heck, Gregory R.
js APPLICANT: La Rosa, Thomas J.
js TITLE OF INVENTION: Plants
js TITLE OF INVENTION: Plants
js TITLE OF INVENTION: Plants
js TILE REFERENCE: 38-21(15309)B
js CURRENT FILING DATE: 2001-10-12
js PRIOR APPLICATION NUMBER: US/09/2563,191
js PRIOR FILING DATE: 1999-03-05
js NUMBER OF SEQ ID NOS: 31255
js LENGTH: 177
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Sequence 4669, Appagequence 1137, Appl Sequence 1137, Appl Sequence 6508, App Sequence 1, Appli Sequence 1, Appli Sequence 7826, App Sequence 761, App Sequence 3175, App Sequence 214, App Sequence 224, App Sequence 244, App Sequence 841, App Sequ
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US-09-540-209B-4669

US-10-1165-299-11327

US-10-105-299-11327

US-10-105-299-6872

US-09-928-531-3

US-09-928-531-3

US-09-928-531-3

US-09-528-531-3

US-09-529-7826

US-09-670-299-7826

US-09-670-209B-768

US-09-640-209B-751

US-09-540-209B-751

US-09-540-209B-751

US-09-540-209B-751

US-09-540-209B-751

US-10-10-299-9443

US-10-015-219-226

US-10-019-219-226

US-10-09-926-254

US-10-09-926-755

US-10-09-926-755
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APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants

RESULT 2
US-09-975-254-11803
Sequence 11803, Application US/09975254
GRNERAL INFORMATION:
APPLICANT: Byrum, Joseph R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10103675

GENERAL INFORMATION:
APPLICANT: Roblson, Keith E.
TITLE OF INVENTION: Nucletc Acid Molecules Encoding Nucleic
TITLE OF INVENTION: Acid and Protein Homologs
FILE REFERENCE: 3800/207402
CURRENT APPLICATION NUMBER: US/10/103,675
CURRENT APPLICATION NUMBER: US/09/749,278
PRIOR APPLICATION NUMBER: US/09/749,278
PRIOR SPLING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%; Score 32.6; DB 6; Length 1206;
11arity 53.5%; Pred. No. 1.9;
Conservative 0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                     Length 250;
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                                                                                                                                                                                                                                                                     DB 5;
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FILE REFERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 11803
LENGTH: 250
                                                                                                                                                   TYPE: DNA
ORGANISM: Glycine max
CHER INFORMATION: Clone ID: 700905274H1
0S-09-975-254-11803
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CORGANISM: Homo sapiens
US-10-103-675-20
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Best Local Similarity
Matches 68; Conserv
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APPLICANT: SELLIAMENT, JOERGRONE, ANGRED M.
APPLICANT: SELVEN, SISSAN G.
APPLICANT: SELVEN, SISSAN G.
APPLICANT: STURE, STREET, STURE, LAURE L.
APPLICANT: WILLIAM, SET G.
THE SERVENCH TOWN MEDICAL TOWN THE STURE CHILD STREET, JOEN THE CONTROL TOWN THE STURE CHILD STREET, JOEN THE CONTROL TOWN THE STURE CHILD STREET, JOEN THE CONTROL TOWN THE STREET, GRAPPED, AND THE STREET, GRAPPED, GRA
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RESULT 6
US-09-540-209B-2484/C
US-09-540-209B-2484, Application US/09540209B
Sequence 2.484, Application
GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: NOCHEN SEQUENCE: 2709.1001-001
CURRENT PERION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 2484
LENGTH: 2004
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                                                           1072 gaacaatcgcccattgtggctgttacaaagacaggtgtgctcttgagtgacggcagcaag 1131
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                                                                                                       538 gtagaagctccattaaatgaagttctggccgccggtatgattttgatgaccggatggaaa 597
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          Indels
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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 1.9%; Score 31; DB 5; Best Local Similarity 52.8%; Pred. No. 7.5; Matches 67; Conservative 0; Mismatches 6
          Mismatches
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ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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          81;
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US-09-974-702-1
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION UNDBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
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Pred. No. 5.5;
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OTHER INFORMATION: Incyte ID No: hu00292960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LCCATION: 89, 188
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-2108-7546
PRIOR FILING DATE: February 13, 1997
PRIOR PAPLICATION NUMBER: 09/035,172
PRIOR PAPLICATION NUMBER: 09/035,172
PRIOR FILING DATE: MARCH 5, 1998
PRIOR FILING DATE: MARCH 5, 1998
PRIOR PELING DATE: MARCH 12, 1998
PRIOR PELING DATE: MARCH 12, 1998
PRIOR PELING DATE: MARCH 14, 1997
PRIOR PELING DATE: MARCH 14, 1997
PRIOR PELING DATE: MARCH 39, 1998
PRIOR APPLICATION NUMBER: 09/050,817
PRIOR APPLICATION NUMBER: 09/074,999
PRIOR PELING DATE: MAY 8, 1998
PRIOR PELING DATE: MAY 9, 1997
PRIOR PELING DATE: MAY 9, 1997
PRIOR PELING DATE: MAY 9, 1997
PRIOR FILING DATE: MAY 9, 1997
PRIOR FILING DATE: MAY 9, 1997
PRIOR FILING DATE: MAY 9, 1997
PRIOR PELING DATE: JULY 1, 1997
PRIOR PELING DATE: JULY 1, 1997
PRIOR FILING DATE: JULR 30, 1998
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NUMBER OF SEQ ID NOS: 35654
SCOFTWARE: PERL Program
SEQ ID NO 7546
LENGTH: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: B.fragilis
US-09-540-2098-2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-540-209B-2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2547
LENGTH: 1365
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507 teattegagigeciggeacgaagaettegaegeagaggeeagagagagtegeegteategg 566
                103 oggectetecgectegetettecgectegaegeagegggaaacggeggegteateatega 162
                                                                                                                                                                                                                                                                                                                                     567 tgccggggccacaagcatccagat 590
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GENERAL INFORMATION:
APPLICANT: Bytum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1290 TGAGAGGCAGGCCAACTTCCTGGGCAAAATCTGGCCCTCCCACAAGGGCAGGCCTGGCAA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   882 tgacaaaaaggccaaccgactggtctatgacttctgggccaaaaagactcgatctcgtat 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 gotocacaggaagcacactcccgcactcccggcctcgccgatttcaacgggaaggtgat 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          942 cgtcaatccggcaaagagagatctcatggctcctctggagccgccgtactggttcgg 998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.9%; Score 30.4; DB 5;
Best Local Similarity 50.7%; Pred. No. 4.5;
Matches 73; Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
CURRENT APPLICATION DATA:

APPLICATION NUMBER: U$/09/974,702
FILING DATE: 09-0Ct-2001
CLASSIFICATION: «UNKNOWN>
PRIOR APPLICATION NUMBER: 09/017,981
FILING DATE: 03-FEB-1998
APPLICATION NUMBER: U$60/037,854
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: GB9705040.5
FILING DATE: 12-WAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.9%; Score 30.6; DE
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19730
TELEPHONE: 732-594-3905
TELEPHONE: 732-594-4720
TELER: «UNFORMATION:
TELER: «UNFOWN: 1:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1532 base pairs
TYPE: nucleic acid
STRANDENESS: double
MOLECULE TYPE: Och
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-974-702-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i TYPE: DNA
) ORGANIZM: Glycine max
) OTHER INFORMATION: Clone ID: 700965057H1
US-09-975-254-25703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-975-254-25703
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APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AND DISTINGUISHING OF
TITLE OF INVENTION: BIOSYNTHETIC LOCI
FILLE REFERENCE: 3001-102
CURRENT APPLICATION NUMBER: US/10/107,431
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 282
SOFTWARE: PATENTLIN Version 3.0
SEQ ID NO 277
           Sequence 182, Application US/10107431
GENERAL INFORMATION:
APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AND DISTINGUISHING C
TITLE OF INVENTION: BIOSYNTHETIC LOCI
TITLE OF INVENTION: BIOSYNTHETIC LOCI
FILE REFERENCE: 3001-70S
CURRENT APPLICATION NUMBER: US/10/107,431
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 282
SOFTWARE: PATENTION OF SED 3.0
SEQ ID NO 182
LENGTH: 3855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1190 tgctggacggcgaccccaaccccgagatcgactgggacggccacgccatccggctggcca 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 tyctccacaggaagcacactcccgcactcccggcctcgccgatttcaacgggaaggtga 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 gtgccggggccacaagcatccagattgttcaggagttggc 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.4; DB 6;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
1.9%; Score 30.4; D
Best Local Similarity 49.4%; Pred. No. 15;
Best Local Similarity 49.4%; Pred. No. 15;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 277, Application US/10107431; GENERAL INFORMATION: APPLICANT: Farnet, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces mobaraensis US-10-107-431-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces mobaraensis
US-10-107-431-277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
US-10-107-431-182
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US-10-107-431-277
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14450 GTTAATTACTCTGATTTCATCATTATACATTATTGACATATATGGAAAAATCACTGTATA 14391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1164 tttcgacagtttcactggctcattgacacatatgggcttgaaaaacaagcacggagtgga 1223
                                                                                                              510 ttcgagtgcctggcacgaagacttcgacgcagagggccagagagtcgccgtcatcggtgc 569
                                    246 tacgccggccgatggcgaggagccgcccggaggctgaggctctggccgcagccgggga 305
                                                                                      570 cggggccacaagcatccagattgttcaggagttggccaagaaggctgaccaggtaaccat
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SEQUENCE 31550, Application US/09540210B
GENERAL INFORMATION:
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: POLJ CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/395,244
PRIOR FILING DATE: Pebruary 27, 1995
PRIOR FILING DATE: Repember 18, 1997
PRIOR FILING DATE: September 27, 1995
PRIOR FILING DATE: September 28, 1995
PRIOR FILING DATE: MATCH 29, 1995
PRIOR FILING DATE: MATCH 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 30; DB 6; Length 32195; ilarity 49.4%; Pred. No. 53; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                      RESULT 12
US-101-102-62/c
US-101-102-62/-92/c
Sequence 92, Application US/10102627
GENERAL INFORMATION:
PAPLICANT: Rosen et al.
TITLE OF INFORTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBACE: PTZ34C1
CURRENT APPLICATION NUMBER: US/10/10/2,627
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 110
FILO Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1224 cctgaaggaggtgtggaaagatggcatatctacttata 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens US-10-102-627-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 78; Conserv
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LENGTH: 32195
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APPLICANT: LAN, Ruth Y.
APPLICANT: URASHKA, MIChael
TITLE OF INVENTION: SECRETORY MOLECULES
CURRENT APPLICATION NUMBER: PCT/USO2/09921
CURRENT APPLICATION NUMBER: E0/280, 068; 60/291,280; 60/291,849;
BRICA APPLICATION NUMBER: E0/200,001; 60/299,776
FRICK FILING DATE: 2001-03-29; 2001-05-16; 2001-05-17;
SOULOS-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 1146
SOFTWARE: PERL PROGram
                                                                       446 tgotocacaggaagcacactecegeaeteceeggeetegeegattteaaegggaaggtga 505
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                506 ttcattcgagtgcctggcacgaagacttcgacgcagagggccagagagtcgccgtcatcg
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
) OTHER INFORMATION: Incyte ID No: LG:116015.2:2001JUN22
PCT-US02-09921-464
                                                                                                                                                                                                                                                                     13886 getacggcggcaccgtggcccacgtcgtcctggagcaggc 13925
                                                                                                                                                                                                                           566 gtgccggggccacaagcatccagattgttcaggagttggc 605
  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Pred. No. 16;
0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 464, Application PC/TUS0209921; GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YU, Jimmy Y.

YDASO, Olivia
YAP, Pierre E.
AMSHEY, Stefan R.
DANGHERTY, Sean C.
DAM, Tam C.
LIU, Tommy F.
NGUYEN, Duy-Viet An
KLEFFELD, Yael
GRESTIN JR., Edward H.
PERALTA, Careyna H.
  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JONES, Anissa L.
TRAN, Alanna-Phung B.
DAHL, Christopher R.
GIETZEN, Darryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHINN, Joyce
DUFOUR, Gerard E.
HILLMAN, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVID, Marie H.
LEWIS, Samantha A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEN, Alice J.
PANZER, Scott R.
HARRIS, Bernard
FLORES, Vincent
MARWAHA, Rakesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8
Best Local Similarity 52.8
Matches 65; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 464
LENGTH: 3188
79;
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APPLICANT:
APPLICANT:
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  Matches
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PRIOR APPLICATION NUMBER: 60/014,010
PRIOR APPLICATION NUMBER: 06/015,33
PRIOR FILING DAME: MATCH 10, 1997
PRIOR FILING DAME: APLI 10, 1997
PRIOR FILING DAME: APLI 110, 1996
PRIOR PELING DAME: APLI 110, 1996
PRIOR PAPLICATION NUMBER: 06/023,308
PRIOR PELICATION NUMBER: 06/023,308
PRIOR PELICATION NUMBER: 06/031,219
PRIOR PELING DAME: MAY 23, 1997
PRIOR PELING DAME: JULY 31, 1996
PRIOR PAPLICATION NUMBER: 06/031,279
PRIOR PELING DAME: JULY 31, 1996
PRIOR PAPLICATION NUMBER: 06/031,279
PRIOR PELING DAME: JULY 31, 1996
PRIOR PAPLICATION NUMBER: 06/032,204
PRIOR PELING DAME: JULY 31, 1996
PRIOR PAPLICATION NUMBER: 06/023,204
PRIOR PELING DAME: JULY 31, 1996
PRIOR PAPLICATION NUMBER: 06/023,204
PRIOR PELING DAME: JULY 31, 1996
PRIOR PELING DAME: JULY 31, 1997
PRIOR PELING DAME: JULY 31, 1996
PRIOR PELING DAME: SUPPEMBER: 06/025, 204
PRIOR PELING DAME: NOVEMBER: 06/025, 204
PRIOR PELING DAME: NOVEMBER: 06/021, 399
PRIOR PELING DAME: NOVEMBER: 06/020, 325
PRIOR PELING DAME: NOVEMBER: 06/020, 325
PRIOR PELING DAME: MATCH 4, 1998
PRIOR PELING DAME: MATCH 4, 1998
PRIOR PELING DAME: MATCH 12, 1999
PRIOR PELING DAME: MATCH 12, 1997
PRIOR PELING DAME: MATCH 13, 1997
PRIOR PELING DAME: MATCH 14, 1997
PRIOR PELI
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RESULT 14

US-09-975-2303/C

SGQUENCE 29303, Application US/09975254

SGQUENCE 29303, Application US/09975254

SGUENCE 29303, Application US/09975254

SGUENCE 29303, Application US/09975254

SAPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

PRIOR APPLICATION NUMBER: US/09/253,191

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 31255

SEQ ID NO 29303

LENGTH: 268
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49.1%; Pred. No. 6.8;
tive 0; Mismatches 82;
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1.8%; Score 29.8; D
Best Local Similarity 50.3%; Pred. No. 7.2;
Matches 73; Conservative 0; Mismatches
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00501861
US-09-540-210B-31550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
): ORGANIENA Glycine max
): OTHER INFORMATION: CLone ID: 700899651H1
US-09-975-254-29303
PRIOR FILING DATE: July 1, 1997
PRIOR APPLICATION NUMBER: 09/094,079
PRIOR FILING DATE: June 9, 1998
PRIOR APPLICATION NUMBER: 60/049,975
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SEQ ID NO 31550
LENGTH: 239
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ORGANISM: Homo sapiens
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### RESULT 15
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### RESULT 1600-299-6650
### RESULT INFORMATION:
### REPRENATION:
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Gencore version 4.5

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OM nucleic · nucleic search, using sw model

Run on: April 26, 2002, 19:22:16; Search time 5001.19 Seconds (without alignments)

A420.550 Million cell updates/sec

Title: US-09-882-694A-2

Perfect score: 1638
Sequence: 1638
Sequence: 1 atgtcggccaccagcaactc......tgcttcatgctccctgctaa 1638
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 0
Maximum Match 100%
Listing first 45 summaries

Database: EST:*
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Dase: EST:\*

| : em\_estba:\*
| : en\_estba:\*
| : en\_esthum:\*
| : en\_esthum:\*
| : en\_estp:\*
| : en\_estp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
	95.4	5.8	544	6	AW180687	AW180687 M9A0835f
7	88.8	5.4	496	12	AQ962221	AQ962221 LERGE08TF
E,	88	5.4	621	φ	AW745217	AW745217 LG1_387_F
4	77.8	4.7	393	0	AT005115	AT005115 AT005115
0	69.4	4.2	596	12	AQ967995	AQ967995 LERIW94TF
9	69	4.2	421	12	AQ967996	AQ967996 LERIW94TR
7	67	4.1	398	σ	AA784433	AA784433 d5q12al.r
80	52.8	3.2	529	10	BI949834	BI949834 HVSME1001
0,	51.8	3.2	498	10	BG507355	BG507355 sac58a01.
c 10	49.2	3.0	546	10	BE760936	BE760936 an_0959 A
11	48	2.9	472	10	BI700307	BI700307 saq66c04.
12	46	2.8	915	10	BF065971	BF065971 HV_CED001
13	45.8	2.8	421	Φ	BE188259	BE188259 PSI35R3 I
14	45.6	2.8	539	6	AA556804	AA556804 646 Loblo
15	44.6	2.7	396	10	BG157908	BG157908 EM1_6_D05
16	44.6	2.7	450	10	BF177238	BF177238 EM1_1_D01
17	44.6	2.7	551	10	BG464165	BG464165 EM1 70 D1

BG465588 EM1_50_D1 BG356283 EM1_23_F0 BF263256 HV_CE9000 BG158097 EM1_8_D10 AQ529083 mbxb000221 BG45509 EM1_60_H0 B14999 EM1_60_H0 B14999 EM1_60_H0 B14996 Sali13f05. BG454500 NF099F031. BG5255 32-7 Stev C97940 C97940 Rice AQ991295 RF602194 AL108460 Drosophil BG526271 58-43 Ste AW267708 EST305836 BH48945 BGCOR49TR AL027269 FUGU LUDT BH48945 BGCOR49TR AL027269 FUGU LUDT BH48945 BGCOR49TR BH48945 BGCOR49TR AL027269 FUGU LUDT BH1914155 GSTF92214	HJ10593 BJ10593 AU208788 AU208788 AU198737 AU198737 BJ107504 BJ107504 BJ150341 BJ150341 C98651 C98651 Rice BM134375 WHE0489_D BE705434 SC02_1290 AV637658 AV637658
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## ALIGNMENTS

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Gaps

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521 303 581

404 183 464

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/organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xr="taxon:3702"
/clone="LERGENO"
/clone=lib="LERG"
/clone=lip="LERG"
/note="Corgan: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4.7 Kbb before ligation."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
Department of Botany
The University of Goorgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                   124 AGTCGATCGCGCGGTGTTCGATGAAAACGCCAATGCCTGGTCGGTGACGTCGTCGGACGG
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                                                                                                                                                                                                        496;
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                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                    5.4%; Score 88.8; DB 12;
50.2%; Pred. No. 5e-14;
ilve 0; Mismatches 242;
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                                                                                                                                                                                                                                           247; Conservative
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Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases 1 to 496)

E Helbyum,T., Liang,F., Creasy,T. and Fraser,C.M.

Genomic survey sequencing of Landsberg erecta ecotype of

Arabidopsis thaliana and identification of sequence-based polymorphisms

Unpublished (2000)

Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Email: ateligr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ962221 496 bp DNA linear GSS 28-JAN-2000 LERGE008TF LERG Arabidopsis thallana genomic clone LERGE00, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: atetigr.org
tor additional information, see http://www.tigr.org/tdb/at/at.html
Seg primer: TF
Class: shotgun.
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                                                                                                                                                                                                                                                              428 GGGTCAAACCATTGCCAACCACTGGAAGGACGGATGCAAAACATCCATGGGAATTGCCAT 487
                                                                                              ccccgaccagcagcaggcctatttcgaagagttgtgggagcgtggggcctttaattttct 854
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                                                         3;
                       Length 544;
                                                         Indels
                   Score 95.4; DB 9;
Pred. No. 7.2e-16;
0; Mismatches 266;
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AQ962221.1 GI:6789922
                 5.8%;
                                      Similarity 49.9
8; Conservative
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USYSTER MUSHROOM.

Syster mushroom.

Bukaryota: Fund; Basidiomycota: Hymenomycetes; Homobasidiomycetes;

Agaricales: Pleurotaceae: Pleurotus.

1 (bases 1 to 393)

See, S., Kink, Lee, K., Kim, K., Yoo, Y. and Lee, C.

Expressed sequences in fruiting body of Pleurotus ostreatus

Unpublished (2001)

Contact: Beomed (2001)

Lontact: Beomed (1001)

Lontact: Beomed (1001)

Lostitute of Agricultural Science and Technology (NIAST)

249 Secoundomy Kweonseonku, Suwon 441707, Korea

Fax: 82-331-290-0399
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                                                                                                                                                                                                                                                                                                                         Email: bgkimyes@rda.go.kr
Submitted through BRIC(Biological Research Information Center)
Korea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1184 cattgacacatatgggcttgaaaaacaagcacggagtggacctgaaggaggtgtggaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .393
/crganism="Pleurotus ostreatus"
/cultivar="ASI 2029"
/cultivar="ASI 2029"
/clone="MFB11-A03"
/clone="MFB11-A03"
/dev_stage="mature fruiting body"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 4.7%; Score 77.8; DB 9;
Best Local Similarity 50.1%; Pred. No. 5.7e-11;
Matches 193; Conservative 0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                http://bric.postech.ac.kr/
uri No. KS105130.
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                   GI:13419973
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AT005115.1
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                                                                                                                                                                                                    /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lih="light Grown 1 (LGI)"
/note="lorgan: 10- to 14-day-old light-grown (greenhouse)
/note="lorgan: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
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                                                         to exclude PolyA, vector and regions threshold for highest quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gagetgaggtggttgatgcgggtatgccagagatetggggcacetggaetgtcaagacgt 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 621;
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                Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exc
below Phred quality 16. The thress
is 20.
Seq primer: JEN REV
High quality sequence stop: 604
POLYA-NO.
                                                                                                                                                                       Location/Qualifiers
  706 542 1860
706 542 1805
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/strain="Landsberg erecta"
/clone="Lexon:3702"
/clone="Lexon:3702"
/clone="Lexon: Lext"
/note="Corgan: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.7 Kbp before ligation."
               AQ967995 59-JAN-2000
LERIW94TF LERG Arabidopsis thallana genomic clone LERIW94, DNA
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                                                                                                                      Arabidopsis thaliana
Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 596)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of polymorphisms
Polymorphisms
Our published (2000)
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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For additional information, see http://www.tigr.org/tdb/at/at.html
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Pred. No. 1.7e-08;
0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                           Contact: Xlaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
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GSS
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AQ967996.1 GI:6795823
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Best Local Similarity 58.5%;
Matches 121; Conservative
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Class: shotgun.
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/organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LBRIWB"
/clone="LBRI
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sposides; eurosidas II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 421)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Fedblyum,T., Liang,F., Creasy,T. and Fraser,C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thallana and identification of sequence-based
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                                                                                                                                                                                                                                                                                                                                                  polymorphisms
Unpublished (2000)
Contact: Xlaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atetigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Seg primer: TR
Class: shotgun.
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Emericella nidulans

Emericella nidulans

Ewkaryota; Fund; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; Emericella.

1 (bases i to 398)

1 (bases i to 398)

Funde, R. and Roe, B.

An Aspergillus nidulans EST Database

Contact: Euroe A. Roe, University of Oklahoma, broe@ou.edu

Advanced Center for Genome Technology, University of Oklahoma
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Pred. No. 1.8e-08;
0; Mismatches 80; Indels
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Best Local Similarity 59.4%;
Matches 117; Conservative
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us-09-882-694a-2\_1.rst

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(Fussing Interceted):

(Insue_type="Spike")

(Insue_type="Spike")

(Abb.host="TUC121"

(Note="Vector: pBluescript SK(-); Site_I: EcoR; Site_2:

(Note="Vector: pBluescript SK(-); Site_I: EcoR; Site_2:

(Note="Vector: pBluescript Sk(-); Site_I: EcoR; Site_2:

(Anote="Vector: pBluescript Sk(-); Site_I: EcoR; Site_2:

(Anote Site Mine Spikes were harvested and snap

(Fozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium

(Graminearum inoculation (Heinen): In the TJ Close lab at

(Toten of Incersity of California, Riverside, total RNA was

(Prepared from each sample pool, equal quantities of all

eight RNA pools were combined, poly(A) RNA was purified

from the mixture, one primary unamplified cDNA library was

made, and I million pfu were in vivo excised to give

pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatras)

). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI

(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main):

The sequence has been trimmed to remove vector sequence

and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                 Activate "Morex"

Ab_xref="taxon:4513"

Aclone_"HVSME10016F16f"

Aclone_"HVSME10016F16f"

(Fusarium infected)

(Fusarium infected)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1052 gegtegaaattgtgaatetagaacaategeeeattgtggetgttacaaagacaggtgtge 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                             /organism-"Hordeum vulgare"
                                                      Total My Dusses - ...
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.7
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                  1.398
/organism="Emericella nidulans"
/strain="FGSC A.56"
/db_xref="taxon:162425"
/db_xref="taxon:162425"
/clone="ds-faspergillus nidulans 24hr asexual
/clone="taspergillus nidulans 24hr asexual
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/clone="taspergillus"
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1 (bases 1 to 529)

Wing, R., Whenlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen 'S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B1949834 1529 bp mRNA linear EST 19-OCT-2001 HVSME10016F16f Hordeum vulgare spike EST library HVcDNA0012 (Fusarium infected) Hordeum vulgare cDNA clone HVSME10016F16f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Contact: Wing RA
                                                                                                        Email: broe@ou.edu
We antidipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gacgecateategttggageeggeeteageggeatetetgetgtgtaeaaattgegaaag 105
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
620 Parrington Oval, Norman, OK 73019,
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                             Seq primer: Sk High quality sequence stop: 342. Location/Qualifiers 1...398
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B1949834.1 GI:16291434
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VERSION
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AUTHORS
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Shoemaker.R., Keim.P., Vodkin.L., Erpelding,J., Coryell,V., Khanna.
A., Bolla,B., Marra,M., Hiller.L., Kucaba,T., Marthi,J., Beck.C.,
Wyller.T., Underwood.K., Steptce,M., Theising,B., Allen,M., Bowers
WY., Person,B., Swaller.T., Gibbons,M., Pape,D., Harvey,N., Schurk
A.Y., Ratesrch.R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
Tal: 314 286 1810
Ear: 314 286 1810
Enail: est@waston.wstl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-331-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="scheen tissue of greenhouse grown plants"
/tissue_type="scheen tissue of greenhouse grown plants"
/dav_stage="scheen tissue of greenhouse grown plants"
/dav_stage="plugges" scheen tissue of pluescript II SK+; Site_1: EcoRI; Site_2:
Anoi: The CDNA library was constructed from mRNA isolated
from stem tissue of 1 month old greenhouse grown plants
for the cultivar Raiden. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dry) sequence with a KhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments were
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DHIOB host cells (GlacoBRL). This library
was constructed in the laboratory of Dr. Randy Shoemaker."
                              acsol/355 498 bp mRNA linear BST 28-NOV-2001 Sacs6801.yl Gm-c1062 Glycine max cDnA clone GENOME SYSTEMS CLONE ID: Gm-c1062-3866 5' similar to TR:Q9SVQ1 Q9SVQ1 HYPOTHETICAL 46.5 RC5073FN ;, mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 acgcagaggccagagagtcgccgtcatcgqtgccgqgggccacaagcatccagattgttc 595
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/organism="Glycine max"
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/db_xref="taxon:3847"
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/clone_lib="Gm-cl062"
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BG507355.1 GI:13477492
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/clone_lib="Aspergillus niger, pxES2 (XhoI-EcoRI)"
/clone_lib="Aspergillus niger, pxES2 (XhoI-EcoRI)"
/note="Vector: pxES2: Site_I: Xho-I; Site_2: EcoRI; cDNA
was synthesized with ZAP kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pxES2 (Invitrogen Corp). This vector
permits expression of our library in yeast. "
140 c 165 g 127 t 8 others
                                                                     546 bp mRNA linear EST 24-OCT-2000 cDNA clone 0959 3', mRNA sequence.
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                                                                                                                                                                                                                      Aspergillus niger.
Aspergillus niger
Aspergillus niger
Eukaryota, Fungi.
Burotilales, Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 546)
Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Aspergillus niges Expressed Sequence Tags
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tsang, A.,
Contact: Tsang, A.,
Dept. of Blology
Concordia University
1455 demaisonmenve Blvd. West, Montreal, Quebec, CANADA, H3G 1M8
Tel: 514-848-3405
Fax: 514-848-4504
Email: tsang@wax2.concordia.ca
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Pred. No. 0.0085;
0; Mismatches 139; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 .546
/organism="Aspergillus niger"
/db_xref="taxon:5061"
/clone="0959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GGCGTGAATGTAAGCGTGACATAAC
Insert Length: 546 Std Error: 0.00
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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BI700307.1 GI:15662936
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(dases 1 to 
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Trace considered overall poor quality This clone is available
Trace considered overall poor quality This clone is available
through: Resden, Invitrogen Corp. 2130 South Memorial Parkway
Huntsville, AL 35801 For further information call: (800)-533-4363
or contact via email: coufresgen.com
Seq primer: -40RP from Glabco
High quality sequence stop: 1.
Location/Qualifiers
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                                                      Context: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
501 ggtgattcattcgagtgcctggcacgaagact---tcgacgcagagggccagaggtcgc
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/db_xref="taxon:384"
/db_xref="taxon:384"
/clone="cENOME SYSTEMS CLONE ID: Gm-c1082-1280"
/clone_lib="Gm-c1082"
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DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (400/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacyl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately Iml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SKH') vector that has been digested with EcoHI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Kelm and Dr. Virginia H. Coryell at Northern Alzona University."
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BF065971.2 GI:13265497
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Burkaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;

Spermatophyta: Magnoliophyta; Liliopsida: Poales: Poaceae; Pooideae
; Triticeae; Hordeun.
; Toalea; Toalea; Toalea; Main, D.
; Ming, R., Close, T.J., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi
; D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mia6) seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
On Oct 17, 2000 this sequence version replaced gi:10842610.
Contact: Wing RA
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//Organism="Hordeum vulgare"
//Organism="Flordeum vulgare"
//Organism="Flordeum vulgare"
//Clone=Tib="Hordeum vulgare seedling green leaf EST
Ilbrary HVCDN04005 [Blumeria challenged]"
//Lisue_Lype="seedling green leaf"
//Lisue_Lype="seedling"
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Total hq bases = 551
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 642.
Location/Qualifiers
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CORGANISM CLAGGROCHUM FILTUND

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us-09-882-694a-2\_1.rst

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57
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E. I (basea Lto 386)
S. Reids, R., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L. H.
An EST database from Sorghum: developing embryos
D. Contect: Cordonnier-Pratt MM
Department of Bocardia
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
                                                                                                               /croanism="Pinus taeda" /croanism="Pinus taeda" /croanism="Pinus taeda" /croanism="Pinus taeda" /croanism="Pinus taeda" /croanism="Costal plain loblolly pine from North Carolina" /clone="6cl1g" -cloholly pine C" /clone=lb-Loblolly pine C" /croe=lb-Lost="Solk" /lab_host="Solk" /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI; /confined from immature xilem from the mixture of four genotypes were used. Oligo-dT prime cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP
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EM1.6_D05.bl_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
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Live 0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           2 others
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,NC, 27695-8008
Tel: 919-515-7800
Email: rosswhet@unity.ncsu.edu
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                                                                                                    Location/Qualifiers
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Matches 102; Conservative
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| SIDSI_gcgdata_hold*geneseqg_emb_I_AA1981.DAT:*
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2902
1 MSATSNBRGDCSVACDAIIV......QICQEKVANWDGFDVLHAPC 545
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result	drong.	Query	Query	EC.	£	Description
					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
1	2902	100.0	545	22	-	Exophiala spinifer
CV	481.5	16.6		22	AAB85324	R. ruber cyclodode
m	262.5	9.0		21	AAY80087	Flavin monooxygena
4	213.5	7.4	535	13	AAW49699	Human flavin-conta
S	210.5	7.3	473	22	AAM39176	Human polypeptide
9	208.5	7.2	550	22	AAM40962	Human polypeptide
7	199.5	6.9	532	19	AAW49700	Human flavin-conta
80	199.5	6.9	594	22	AAM79793	Human protein SEQ
6	192.5	9.9	558	22	AAM78809	Human protein SEQ
10	184	6.3	434	22	AAG92928	C qlutamicum prote
11	170.5	5.9	532	17	AAR97549	Human flavin-conta

Novel polynucleotides encoding Exophiala degradative or transport

Duvick JP, Maddox J, Gilliam J, Folkerts O, Crasta OR;

WPI; 2001-147345/15. N-PSDB; AAD02690, AAD02691.

(PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.

99WO-US15824. 99WO-US15824.

14-JUL-1999; 14-JUL-1999;

25-JAN-2001.

Exophiala spinifera WO200105980-A1.

	12		70	286	22	AAB93890	Human protein segu
	13	161.5	2.6	95	21	6	exanone
	14	161	5.5	568	22	ABG21986	Novel human diagno
	15	156.5		416	22	ABB59569	Drosophila melanog
	16	153		219	22	AAB79223	Corynebacterium gl
	17	151	•	450	22	AAU33718	U2
	8 6	150.5	 	342	55	AAG91411	
	7 6	4	•	390	77	4AG92804	c gracamicum proce
	202	146.5		42.4	7 0	ABB59688	Dronionibacterium
	77	, r		4.5	27	ABG40334	arabidoneis thalia
	3 6	143.5		342	10	AAGROOS	
	24	43		342	22	AAG80036	
	25	42		452	21	AAG13800	
	26	42		459	21	AAG13799	
	27	137.5		461	21	AAG46666	bidopsi
	28	m	•	326	18	AAW21022	pylori
	53	125	4.3	312	22	AAU00834	S. aureus thioredo
	30		4.3	311	20	AAY29854	Staphylococcus aur
	31	123.5	4.3	88	21	AAB02093	Cyclohexanone mono
	32	122	4.2	345	22	AAB96222	Putative P. abyssi
	33	122	4.2	206	20	AAY01313	Glutamine-oxogluta
	34	122	4.2	909	22	AAG89954	lutamicum p
	35	120.5	4.2	455	20	AAY29930	N. asteroides stra
	36	118	4.1	85	21	AAB02092	Cyclohexanone mono
	37	117.5	٠	1396	22	ABG29766	Novel human diagno
	38	116	•	73	21	AAB02094	Cyclohexanone mono
	39	116	•	570	21	AAY67416	
	40	116	•	623	21	AAG39829	Arabidopsis thalia
	41	116	4.0	638	21	AAG39828	
	42	116	•	658	21	AAG39827	tha
	43	'n	4.0	203	15	AAR47583	NADH oxidase. Amp
	44	113.5	•	310	20	AAY29855	taphylococcus
	45	e .	٠	310	22	AAG82024	S. epidermidís ope
						ALIGNMENTS	
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AAY	AAY72634	ı					
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ž č	EXO	exopniala sp	spinitera		11 III	ilavin monooxygenase, a iumonisi	rumonisin degradative enzyme,
¥ 3	i i	iniein.	tebenne	9	7 TAY 10	Rumonisin, dearsdative ensume: transport ensume: fla	flavin monooxvgenase:
2 3	2 John 2	hyde deh	od road	3 0 0 0	7 7 9 0	nisport enzyme, n-alveoprofein:	win monoayyendee,
KW	deto	detoxification: mycotoxin: animal	DAE: 100	otoxi			
K	tran	transgenic plant;	lant; t	ransa	enic	al; microbial	
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RESULT AAB85324

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The patent discloses novel polynucleotides encoding Exophiala spinifera

[Limonisin degradative or transport enzymes such as flavin monooxygenase,

[Limonisin degradative or transport enzymes such as flavin monooxygenase,

[Limonisin degradative or transport enzymes such as flavin monooxygenase,

[Limonisin degradative or processed or an enzyme is useful for

[Limonisin or a structurally related mycotoxin present in

[Limonisin on application to a plant or to harvested grain

[Limonisin or to processed grain that is to be used as animal

[Limonisin or as a slidge. Nucleotide fragments of the present

[Limonisin or useful as probes and primers. They can be introduced

[Limonicorganisms that multiply on plants to deliver enzymes to

[Limonicorganisms that multiply on plants to deliver enzymes to

[Limonicorganisms that multiply on plants to deliver enzymes to

[Limonicorganisms that multiply on plants to deliver enzymes to

[Limonicorganisms that multiply on plants to deliver enzymes to

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[Limonicoluced via the environment, plants or animals for reducing the

[Limonicoluced and used as an incrobial host and the resulting bacteria

[Limonicoluced and used as an incrobial host and the resulting bacteria

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ARVDSETPFYQLNIPEVWKDWTWSCRYPDQKELLSYVHHCDKIRGLRKDVYFGAEVVDAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YARDLGTWTVKTSAGHVATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDFDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACQYREVMVDKKANR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIVAVTKTGVLLSDGSKRECDTIVLATGFDSFTGSLTHMGLKNKHGVDLKEVWKDGISTY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present protein sequence is flavin monooxygenase, a fumonisin degradative enzyme from Exophiala spinifera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2902; DB 22; Length 545; 100.0%; Pred. No. 1.3e-273; Live 0; Mismatches 0; Indels 0;
                                                                                     Claim 1c; Page 65-67; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 545; Conserv
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541 lhapc 545

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The invention relates to genes from Rhodococcus ruber involved in cyclododecanone degradation pathway. A 10 kb cluster from R. ruber was isolated that comprises genes (designated cddb, cddb, cddx, cddx, cddx, cddx, cdds, cddb, cddb, cddx, cddx, cddx, cddv, cddc, and cddb) encoding parames such as dodecanoic diacid synthesizing enzyme, cyclododecanone monoxygenese, lauryl lactone esteraes, 12-hydroxylauric condition of dehydrogenese, 12-you lauric acid dehydrogenese, 14-ydroxylauric acid dehydrogenese, 12-you lauric acid dehydrogenese, Host cells conditioned with cyclododecanone, lauryl lactone when contacted with cyclododecanone, 12-hydroxy lauric acid when contacted with lauryl lactone when contacted with cyclododecanone, 12-hydroxy lauric acid when contacted with lauryl lactone when contacted with cyclododecanone, cyclododecanone and cyclododecanone by contacted with a cyclododecanone cyclododecanone by chocyclododecanone cyclododecanone monoxygense enzyme isolated from a lokb nucleic acid fragment from R. ruber SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                Cyclododecanone, degradation; lauryl lactone esterase; cddh, cddB, cddX, dodecanone monooxygenase; cyclic ketone; cddY; 12-hydroxylauric acid dehydrogenase; 12-oxo lauric acid dehydrogenase; macrolactone; microbiological; cddC, cddb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids encoding dodecanoic diacid synthesizing enzyme, cyclododecanone monooxygenase for bioproduction of dodecanoic diacid
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16 6%; Score 481.5; DB 22;
Best Local Similarity 26.4%; Pred. No. 9.6e-38;
Matches 153; Conservative 85; Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson KJ, Kostichka KN,

    R. ruber cyclododecanone monooxygenase enzyme.

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AAB85324 standard; Protein; 603
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                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000; 2000WO-US33426.
                                                                                      (first entry)
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N-PSDB; AAH22871.
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                                                                                                                                                                                                                                                                                   Rhodococcus ruber.
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                                                                                      17-SEP-2001
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                                           AAB85324;
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New isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters, used for detoxifying fumonisin or related mycotoxin or reducing the pathogenicity of fundi producing fumonisin -
                                                                                                                                                                                                                                                                           135 GHVATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDF·--DAEG-----Q 183
                                                                                                                            236 rvavigtgatavqcvpelakycrelyvvqrtpsavdergnhpidekwfaqiatpgwqkrw 295
                                                                                                                                                        ----APSVGIFEVSPEQREAYFEE 275
                                                                                                                                                                               296 ldsftaiwdgvltdpselaiehedlvqdgwtalggrmraavgsvpiegyspenvgralee 355
                                                                                                                                                                                                         276 LWERGAFNFLACOYREVMVDKKANRLVYDFWAKKTRSRIVNPAKRDLMAPLEPPYWFG-- 333
                                                                                                                                                                                                                                  356 ------addegmeri----rar-vdeivtdpataaglkawfrqm 388
                                                                                                                                                                                                                                                                                                               393 TGSLTHMGL--KNKHGVDLKEVWKDGISTYMGVFSHGFPNAFFVATAQAPTVLSNGPTII 450
                                                                                                                                                                                                                                                                                                                               KDWTWSCRYPDQKELLSYVHHCDKIRGLRKDVY----FGAEVVDARYARDLGTWTVKTSA 134
                                                                                                                                                                                                                                                         334 TKRSPLESDYYEMLDKPSVEIVNLEQSPIVAVTKTGVLLSDGSKRECDTIVLATGFDSF-
                                                                 RVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYC-----LPMRQRTMDRNEQTAWKAYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterium 2412.1; maize; detoxification; degradation; carcinogen; fumonisin catabolic gene cluster; antifungal; mycotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavin monooxygenase fccC amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                               451 ETQVDLIADTIAKLEAEHATSVEATKSAQEAWSIMI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                              602
                                                                                                                                                                                                                                                                                                                                                                                                                   488 KMNEH------TLFPLTDSWWTGGNIPGKATRALTF 517
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                                                                                                                                                       239 PTLFEASRKSRIGFPVQ-----
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The present invention describes isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters from a school content of Marchian Catabolic gene cluster. The Bacterium 2412.1 content was isolated from maize. The nucleic acid molecules can be used for producing an enzyme for detoxifying fumonisin or a structurally related converted grain, or processed grain which is to be convected an animal feed or silage. Runninal microorganisms transformed with the nucleic acid molecules can be used as probiotic compositions or as feed incoulant compositions. Plants transformed with the nucleic acid molecules can be used as probiotic compositions or as feed incoulant compositions. Plants transformed with the nucleic acid molecules can degrade or transport fumonisin. The plants may be e.g. maize, sorghum, wheat, tomach, soybean, alfalfa, sunflower, Brassica, cotton or rice. The products can also be used as detection reagents for fumonisins and related compounds. AAS91253 represents the Bacterium for Catabolic gene cluster, and AAS91254 to AAS91273 crepresent isolated nucleic acids from Bacterium 2412.1 which encode AAS90085 to AAY801286 from Bacterium 2412.1 which encode campulfication of the present invention. AAS91274 to AAS91285 are given in the sequence listing from the present specification but are not seven the present specification but are not seven to the present specification but are not seven to the present specification but are not seven to the present sequence are seven to the present specification but are not seven to the present sequence are seven to the present sequence are set in the sequence are seven to the present specification but are not seven to the present sequence are seven to the present sequence are seven to the present sequence are set in the sequence are seven to the present sequence are seven to the pres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 ------mhdfgedgtgmplkylrrasgyyidvgasellas-----gaiklrsr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 LESDYYEMLDKPSVEIVNLEQSPIVAVTKTGVLLSDGSKRECDTIVLATGF---DSFTGS 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 QRVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQRTMDRNEQTAWKAYYPTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 IIVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFY-----QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 pfpdtwpvytpkdkigdwleayaqamell-------vwcstrcvsavydaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTWTVKTSAGH -- - VATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDFDAEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 9.0%; Score 262.5; DB 21; al Similarity 23.6%; Pred. No. 1.8e-16; 105; Conservative 57; Mismatches 163;
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This sequence represents the human flavin-containing mono-oxygenase isoform 2 (hPWO2) protein. The coding sequence (AAV57273) was isolated as a genomic clone (AAV57272) from a bacterial artificial chromosome as a genomic clone (AAV57272) from a bacterial artificial chromosome (BAC) library covering the complete human genome. Clone BAC 123804M was isolated using STS probes and markers based on human chromosome 1 (the filorescence in situ hybrdisation). The BAC clone was digested with restriction enzymes. The fragments were subcloned and the inserts sequenced. The human FWO sequence was identified by homology to known FWO sequences. Fragments of the FWO2 sequence can be used as primers or probes specific for particular alleles, especially the G.1263mac.A mutation. Detection of this mutation allows diagnosis of a predisposition to FWO-associated diseases, particularly the G.1263mac.A mutation allows diagnosis of a predisposition to FWO-associated diseases, particularly where apoptosis is involved, or central nervous system degeneration. Other FWO-related disorders are central nervous system degeneration. Other FWO-related disorders are excessive or inadequate oxidation/metabolism of drugs, toxic xenobiotics or carcinogens. The proteins and cells expressing them can also be used for the blosynthesis/blodegradation, particularly decoxification, of senobiotics (pesticides, herbicides, alabelmaceuticals) and pharmaceuticals) and synthesis of pharmaceuticals, food additives, pesticides and herbicides.
fluorescence in situ hybridisation; homology; primer; allele; mutation; detection; diagnosis; Juvenile wide-angle primary glaucoma; stress; drug; apoptosis; central netrous system; depencration; oxidation; metabolism; xenobiotic; carcinogen; biosyrhhesis; biodegradation; detoxification; pesticide; herbicide; alkaloid; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding iso-forms 2 and x of human flavin-containing mono-oxygenase - useful for diagnosis, treatment and prevention of, e.g. wide-angle primary glaucoma and for synthesis and degradation of compounds
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                 /label- unknown
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N-PSDB; AAV57273.
                                                                                                                                                                                           Misc-difference 472
                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                Homo sapiens
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Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; perlpheral nervous system; neuropathy; central nervous system; CNS; Alzahemer's; Parkinson's disease; huntington's disease; haemostatic; amyotrophic lateral scletrosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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302 VYDFWAKKTRSRIVNPAKRDLMAPLEPPYWFGTKRSPLESDYYEMLDKPSVEIVNLEQSP 361
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                                       TWTVKT-SAGHVATAKY--LILATGLLHRKHTP--ALPGLADFNGKVIHSSAWHEDFDAE
                                                                  124 qwkvvtqsngkeqsavfdavmvcsghhilphiplksfpgmerfkgqyfhsrqykhpdgse
                                                                                                                                                                                  222 ---srisedgyp-----wdsvfhtrfrsmlrnvlprtavkwmieggmnr-
                                                                                                182 GORVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQRTMDRNEQTAWKAYYPTL
                                                                                                               242 FEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACQYREVMVDKKANRL
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Zhang J;
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Yang Y,
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such as central nervous system injuries
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25-APR-2000; 2000US-0552317,
09-UL-2000; 2000US-059042.
19-JUL-2000; 2000US-0620312.
03-AUC-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
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Zhao QA,
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7.4%; Score 213.5; DB 19; 22.6%; Pred. No. 1e-11; ve 62; Mismatches 159; 3

22.6%;

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79 KDWTWSCRYPDQKELLSYVHHCDKIRGLR------KDVYFGAEVVDARYARDL---G 126

IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78

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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous systems, such as peripheral nervous injuries, peripheral nervous shalted nervous systems, such as as a lateral sclerosis, and shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune systems suppression, Activin/inhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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Pred. No. 1.7e-11;
L; Mismatches 160;
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Local Similarity 22.6%; Protes 89; Conservative 61;
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM48642-AAM42213) with nootropic, humunosuppressant and oytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, and as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic aleater's, Parkinson's disease, Huntington's disease, amyotrophic disease, special sclenosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukemias and constants.
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Zhang J;
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                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.2%; Score 208.5; DB 22; 22.6%; Pred. No. 3.3e-11; tive 60; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                               hen R, Ma Y, C
Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 5893; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Xu C,
                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                               Liu C, Asundi V, Che
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
                                                                                                     29-UL-2000; 20000S-0598042;
19-UL-2000; 20000S-059812,
03-AUG-2000; 20000US-065315,
14-CFT-2000; 2000US-0653150,
19-OCT-2000; 2000US-0693036,
29-WOV-2000; 2000US-0593036,
26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification.
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89;
                                                                                                                                                                                                                                                                                                                                                                                               Wang J, W
                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
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13;

532 AA;

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for the blosynthesis/blodegradation, particularly detoxification, of xenoblotics (pesticides, herbicides, alkaloids and pharmaceuticals) and synthesis of pharmaceuticals, food additives, pesticides and herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human flavin-containing mono-oxygenase isoform x (hFMOX) protein. The coding sequence (AAV57275) was isolated as a genomic clone (AAV57274) from a bacterial artificial chromosome as a genomic clone (AAV57274) from a bacterial artificial chromosome (BAC) library covering the complete human genome. Clone BAC 123HQAM was solved using 575 probes and markers based on human chromosome 1 (the gen's location was confirmed as being in the region 1423-q25 by fluorescence in situ hybridisation). The BAC clone was digested with restriction enzymes. The fragments were subcloned and the inserts restriction enzymes. The fragments was identified by homology to known FMO sequences. Fragments of the FMO2 sequence can be used as primers or probes specific for particular alleles, especially the G.1263mac.A mutation. Detection of this mutation allows diagnosis of a predisposition to FMO-associated diseases, particularly juvenile function of this mutation allows diagnosis of a predisposition to FMO-associated diseases, including toxic and degenerative disorders, particularly where apoptosis is involved, or central nervous system degeneration. Other FMO-related disorders are central nervous system degeneration. Other FMO-related disorders are excessive or landequate oxidation/metabolism of drugs, toxic xenobities or carcinogens. The proteins and cells expressing them can also be used
                                                                                                                                                                                                                                                                              Human; flavin-containing mono-oxygenase; FWO; BAC; STS; probe; FISH; bacterial artificial circomosome; sequence tagged site; chromosome; fluorescence in situ hybridisation; homology; primer; allele; mutation; detection; diagnosis; juvenile wide-angle primary glaucoma; stress; drug; apopticis; central nervous system; depenaration; oxidation; metabolism; xenoblotic; carcinogen; biosynthesis; blodegradation; detoxification; pesticide; herbicide; alkaloid; food additive.
     ----wfnhen-----yglepqnkyimkepvlnddvpsrllcgaikv----kst 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding iso-forms 2 and x of human flavin-containing mono-coyygenase - useful for diagnosis, treatment and prevention of e.g. wide-angle primary glaucoma and for synthesis and degradation of compounds
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                                                                                                                                                                                                                                                 Human flavin-containing mono-oxygenase isoform x.
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                    362 IVAVTKTGVLLSDGSKRE-CDTIVLATGFDSFT 393
                                                     /note- "encoded by NAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                AAW49700 standard; peptide; 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-FR02226.
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                                                                                                                                                                                                                    (first entry)
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N-PSDB; AAV57275.
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     278
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                                                                                                                                                                                                                                                                                                                                                                                                                         226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                                                                                                                         170 HSSAWHEDFDAEGQRVAVIGAGATSIQIVQELAKKADQVTMFWRRPSYCLPMRQRTMDRN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 ksrn-----nevtlfkgifpplmekptlaviglvgslgaaiptadlgawwaakvfa 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 K-----DWTWSCRYPD-------QKELLSYVHHCDKIRGLRKDVYFGAEV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 sdwlyvqkmnt----wfkhenyglm------pingslrkepvfndelpsril 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 -- EMLDKPSVEIVNLEQSPIVAVTKTGVLLSDGSKREC-DTIVLATGFDSFTGSLTHMGL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 cgtlsikpsvk-----eftetsavfedgtmfealdsvifatgydysypfldetim 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNKHGVDLKEVWKDGISTYMGVFSHGF--PNAFFVATAQA----PT-----VLS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 NGPTIIETQVDLIADTIAK------LEAEHATSVEATKSAQEAWSIMIAKMNE 491
                                                                                           19 IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78
                                                                                                                                                                                                                                                                                                          117 VDARYARDLGTWTVKTSA-GHVATAKY--LILATGLLHRKH----TPALPGLADFNGKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 EQTAWKAYYPTLFEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dgypwdmnyvtrfasflr----nvlpsfl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 REVMVDKKANRLVYDFWAKKTRSRIVNPAKRDLMAPLEPPYWFGTKRSPLESDYY----
                                                 Indels 167;
  Length 532;
  DB 19;
6.9%; Score 199.5; DB 19;
21.0%; Pred. No. 2.3e-10;
ative 80; Mismatches 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein SEQ ID NO 3439.
                          Similarity 21.0%
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 pwif-itd 454
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                                                 Matches 115;
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     Query Match
Best Local S
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy, The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity is useful may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                 Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer, leukaemia; nervous system disorder; arthritis; inflammation.
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299 fnhedyglsitkgkkakfivndelpncilcgaitmktsvieftetsavfedgtveenidv 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 558;
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Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 3746-3747; 6221pp; English.
                                                                                                                                                                                                      AAM78809 standard; Protein; 558 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-2000, 2000US-0496914.
27-APR-2000; 2000US-0560B75.
20-JUN-2000; 2000US-059075.
19-JUL-2000; 2000US-053335.
11-SEP-2000; 2000US-0554936.
20-OCT-2000; 2000US-0654936.
30-NOV-2000; 2000US-0633251.
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                                                                                                                                                                                                                                                                                                                                               Human protein SEQ ID NO 1471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US04098
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                                                                                 359 vifttgy 365
                                               383 IVLATGF 389
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                   AAM78809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78123-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, accines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodilatory activity and activity is and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 miwplalslirhggfcysdfpfhedypnfmnhekfwdylgefaehfdilkyigfkttvcg 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 LRKDVYFGAEVVDARYARDLGTWTVKTSA---GHVATAKYLILATGLLHRKHTP--ALPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 LADFNGKVIHSSAWHEDFDAEGQRVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 MRQRTMDRNEQTAWKAYYPTLFEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 AFNFLACOYREVMVDKKANRLVYDFWAKKTRSRIVNPAKRDLMAPLEPPYWFGTKRSPLE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- OSPIVAVTKTGVLLSDGSKRE-CDT 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy ^{\circ}
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                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 6.9%; Score 199.5; DB 22; Length 594; Local Similarity 20.1%; Pred. No. 2.8e-10; hes 86; Conservative 61; Mismatches 149; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 336; 6221pp; English.
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                                                                    27 APR 2000; 2000US -0560875.
20-20N-2000; 2000US -059075.
19-JUL. 2000; 2000US -0621325.
01 SEP -2000; 2000US -0654936.
15-SEP -2000; 2000US -0653561.
20-OCT -2000US -0693253.
     35-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476283/51.
N-PSDB; AAK$2926.
                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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Matches
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17 - NOV - 1995;
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                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                             121 -----etgqwdvvtetegkqnravfdavmvctghflnphlpleafpgihkfkgqilhs 173
                                                                                                                                      231
                                                                                                                                                                                                               292 VMVDKKANRLVYDFWAKKTRSRIVNPAKRDLMAPLEPPYWFGTKRSPLESDYYE----M 346
                                                        79 KD-------WIWSCRYPDQKELLSYVHHCDKIRGLRKDVYFGAEV 116
                                                                           64 kemscysdfpfhedypnfmnhekfwdylgefaehfdlikyigfkttvcsitkrpdfs--- 120
                                                                                              117 VDARYARDLGTWTVKTSA---GHVATAKYLILATGLLHRKHTP--ALPGLADFNGKVIHS 171
                                                                                                                                                         221
                                                                                                                                                                         232 TAWKAYYPTLFEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACQYRE 291
                                                                                                                                                                                             -----ynnm----- 234
                                                                                                                                                                                                                            19 IVGAGLSGISAVYKLRKLRLANAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                 172 SAWHEDFDAEGORVAVIGAGATSIQIVQELAKKADOVTMFMRRPSYCLPMRQRTMDRNEQ
                                                                                                                                                                                                                                                     347 LDKPSVEIVNLE------QSPIVAVTKTGVLLSDGSKRE-CDTIVLATGF 389
                                                                                                                                                                                                                                                                  Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
  Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO: 6682; 246pp + Sequence Listing; English.
 139;
                                                                                                                                                                                                                                                                                                                                                                                C glutamicum protein fragment SEQ ID NO: 6682.
 Mismatches
                                                                                                                                                                                                                                                                                                                      AAG92928 standard; Protein; 434 AA
 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0377484
                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
 Conservative
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07-APR-2000;
03-AUG-2000;
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 81;
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Tateishi N,
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Matches
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18;
are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, uncleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 184; DB 22; Length 434;
21.2%; Pred. No. 5.56-09;
Live 68; Mismatches 164; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 V---KTSAGHVATAKYLILATGLLHRKHTPALPGLADFNGKVIHSSAWHEDFDAE-GORV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQRTMDRNEQTAWKAYYPTLFEAS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 vvlgannsahdicadlysngakpvmigrssthiv-----rsdslmrevfgp----- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 RKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACQYREVMVDKKANRLVYDF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----idtdtadllfas 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 wpykvlpgvqkqafdkireddkefydklenagflldfgdddsglflkylrrgsgyy--1d 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 KPSVEIVNLEQSPIVA-----VTKTGVLLSDGSKRECDTIVLATGF---DSFTGSLTHM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 IIVGAGLSGISAVYKLRKLRKLRAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPE- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 VWKDWTWSCRYPD-----OKELLSYVHHCDKIRGLRKDVYFGAEVVDARYARDLGTWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 WAKKTRSRIVNPA------KRDLMAPLEPPYW---FGTKRSPL------ESDYYEMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monooxygenase; flavin; xenobiotic; carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|: :|}
361 etadkvgpcwglgsettkdpgpwegelrnmwk 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 GLKNKHGV------DLKEVWK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human flavin-containing monooxygenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 21.29
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      434 AA;
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The present invention describes primer sets for synthesising 5602 (full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an olligoucleotide complementary to the complementary strand of a polynucleotide which complementary comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of complementary strand of a polynucleotide comprises a 3'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence and an oligonucleotide which comprises a 3'-end sequence is selected from those defined in the 5'-end sequence. The primer sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and configuration and/or diagnosis of the abnormality of the proteins encoded by compared the primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for AMH13628 and AMH13633 to AAHH3642 represent human amino acid sequences; AMB92446 to AMH13632 to AAHH3639 to AAHH3639 to AAHH3639 to AAHH3639 to AAHH3639 to be present human amino acid sequences; and AAHH3629 to hall invention of the present companies of the aventual of the useful invention of the present companies of the aventual of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 KDWTWSCRYPDQKELLSYVHHCDKIRGLR------KDVYFGAEVVDARYARDL---G 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 kemmcfsdypipdhypnfmhnagvleyfrmyakefdllkyirfkttvcsvkkqpdfatsg 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 TWTVKT-SAGHVATAKY--LILATGLLHRKHTP--ALPGLADFNGKVIHSSAWHEDFDAE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 GQRVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQRTMDRNEQTAWKAYYPTL 241
gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGARVDSETPFYQLNIPEVW 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134; Indels
detection; diagnosis; antisense therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 13827; 2537pp + CD ROM; English.
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5.6%; Score 163.5; DB 2;
Best Local Similarity 22.2%; Pred. No. 2.9e-07;
Matches 70; Conservative 50; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                   Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                        Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                     Nishikawa T,
                                                                                                                                                                                                    29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
1-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-018376.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                            28-JUL-2000; 2000EP-0115126
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                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 AA;
  Human; primer;
                                          Homo sapiens.
                                                                               EP1074617-A2
                                                                                                                       07-FEB-2001
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                                                                                                                                                                                                                                                                                 A novel for human flavin-contg. monooxygenase (AAR97549) is a microsomal enzyme that oxidises xenobiotics such as drugs, agrochemicals and environmental pollutants. The recombinant enzyme can be obtd. by expression in Saccharomyces cerevisiae host cells transformed with e.g. vector pAFMO carrying the monooxygenase gene (AA731804). The enzyme is useful for metabolising test code. to determine whether they are converted to harmless metabolites or to carcinogens. It can also be used to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 --YPGARVDSETPFYQLNIPEVWKDWTWSCRYPDQKELLSYVHHCDKIRGLRKDVYFGAE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| ; | ; | ; | ; ; ; | ; ; ; | ; ; ; ; | mcfpdffpfpddfprfmhns----kiqeyilafakeknllkyiqfktfvssvnkhpdfat- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 -ypwdmllvtrfgtflknnlptaisdwlyvkgmnarfkhenyglmplngvlrkepvfnde 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                            Nucleic acid encoding human flavin contg. monooxygenase – useful for metabolising test cpds. to determine whether they are converted to harmless metabolites, or activated to carcinogens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVDARYARDLGTWTVKTSA-GHVATAKY--LILATGLLHRKHTP--ALPGLADFNGKVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 SSAWHEDFDAEGQRVAVIGAGATSIQIVQELAKKADQVTMFMRRPSYCLPMRQRTMDRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 REVMVDK-----KANRLVYDF------WAKKT-RSRIVNPAKRDLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 APS----VGIFEVSPEQRE----AYFEE-----LWERG---AFNFL-----ACQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 5.9%; Score 170.5; DB 17; Length 532; Local Similarity 20.4%; Pred. No. 1.6e-07; Local Similarity 62; Mismatches 159; Indels 139; los 92; Conservative 62; Mismatches 159; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 IVGAGLSGISAVYKLRKRRRAKIFEGAPDFGGVWHWNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 PLEPPY----WFGTKRSPLESDYYEMLDKPS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:13827.
                                                            Hayashi K, Matsuki Y, Yabusaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 QTAWKAYYPTLFEASRKSRIG-----
                                                                                                                                                                                                                                              Claim 1; Page 8-11; 15pp; English.
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                     (SUMO ) SUMITOMO CHEM CO LID.
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                                                                                                  WPI; 1996-288432/30.
N-PSDB; AAT31804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 AA;
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A new method to identify differentially expressed prokaryotic genes using a large number of arbitrarily primed polymerase chain reactions comprises separating two populations of microbial cells, where a first population is contacted with a stimulating agent; where a first population is contacted with a stimulating agent; extracting total RNA from both microbial cell populations; amplifying the extracted RNA from both populations by preparing a collection of at least thirty-two different arbitrary primers, where collection of at least thirty-two different arbitrary primers, where contacting each primer conditions where two sets of amplification products are produced; purifying the amplification products generated in the products; identifying the amplification products generated from the second population as differentially expressed genes; and optionally second population as differentially expressed genes; and optionally sequencing the identified differentially expressed genes; and optionally differential display to clone genes using thirty-two or thirty or the wmethod using a greater number of primers has isolated four and one genes, respectively. The new method using a greater number of primers has isolated
                    222
                                                    300
                                                                        223 ---nrvgdygypa------dvlfssrlthf--iw-klcgqslanky----lekkingr 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Differential display method using a large number of arbitrary primers for RT-PCR used to isolate novel differentially expressed prokaryotic
                                                  242 FEASRKSRIGFPVQAPSVGIFEVSPEQREAYFEELWERGAFNFLACQYREVMVDKKAN-R
                                                                                                                                                                                                                                                                                                                                                                                   Identification; prokaryote; polymerase chain reaction; PCR; amplification; primer; differential display; picric acid degredation; gene cluster; open reading frame; ORF; dehydratase; dehydrogenase; transcription factor; cyclohexanone monooxygenase.
Cyclohexanone monooxygenase sequence.
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                                                                                                                                                                                                                                            AAB02090 standard; Protein; 95 AA.
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                                                                                                                      301 LVYDFWAKKTRSRIV 315
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                                                                                                                                                                                                                                                                                 AAB02090;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynerleotides and in recombinant production of (II). The colynucleotides are also used in disponsitios as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) is useful for generating antibodies against it, detecting or to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inmeding of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on bus and amino acid sequences. Agains patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
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                                                                          450 IETQVDLIADTIAKLEAEHATSVEATKSAQEAWSIMIAKMNEHTLFPLTDSWWTGGNIPG 509
                                       1; Gaps
                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
  DB 21; Length 95;
                                       Indels
                                     40,
  5.6%; Score 161.5; DB 37.0%; Pred. No. 8.7e-08 ive 17; Mismatches 46
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                                                                                                                                                     510 KATRALTFIGGIALYEQICQEKVA-NWDGFDV 540
                                                                                                                                                                                          94
                                                                                                                                                                             Novel human diagnostic protein #21977.
                                                                                                                                                                                                                                                                                      ABG21986 standard; Protein; 568 AA
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                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Query Match
Best Local Similarity 37.0
Matches 34; Conservative
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N-PSDB; AAS86173.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLG176-ABL3051), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins (ABS7737-AB972072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions –
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 IVGAGLSGISAVYKLRKLRLNAKIFEGAPDFGGVWHWNRYPGA--RVDSETPFY---QLN 73
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                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 5499; 21pp + Sequence Listing; English
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at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APPLICANT: Maddox, Joyce
APPLICANT: G11)iam, Jacob
APPLICANT: G11)iam, Jacob
APPLICANT: G11)iam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Compositions and Methods
TITLE OF INVENTION: Detoxification
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224E
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                               Query Match 100.0%; Score 1638; Best Local Similarity 100.0%; Pred. No. 0; Matches 1638; Conservative 0; Mismatches
                                                                                                           and Methods
                                                                                                                                                                                    COTHER INFORMATION: flavin monooxygenase, US-09-351-224E-2
                                                                    ; Sequence 2, Application US/09351224E; GENERAL INFORMATION:
                            TYPE: DNA
ORGANISM: Exophiala spinifera
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                                                                                                                                                                    DB 17;
                                                         Sequence 2, Application US/09351823
Sequence 2, Application US/09351823
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for FILE REPERENCE: 5718-67
CURRENT APPLICATION NUMBER: US/09/351,823
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                    Query Match 100.0%; Score 1638; DE Best Local Similarity 100.0%; Pred. No. 0; . Matches 1638; Conservative 0; Mismatches
                ORGANISM: Exophiala spinifera
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US-09-677-488A-2
Sequence 2, Application US/09677488A
GENERAL INFORMATION:
APPLICANT: Divick, Jon
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
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                                                                                         OTHER INFORMATION: flavin monooxygenase, fully spliced cDNA
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    Sequence 2, Application US/09677488
Sequence 2, Application US/09677488
GENERAL INFORMATION:
APPLICANT: DUVICK,
TILLE OF INVENTION: Compositions and Methods for Funn:
FILLE REFERENCE: 38718/204100 (5718-111A)
CURRENT APPLICATION UNMER: US/09/677,488
CURRENT FILING DATE: 2000-10-02
PRIOR PILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1638
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                                                                                                                         0; Mismatches
                                                                                                             100.0%; Score 1638; 100.0%; Pred. No. 0;
                                                                          TYPE: DNA
ORGANISM: Exophiala spinifera
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Best Local Similarity 100.
Matches 1638; Conservative
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US-09-677-488-2
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Sequence 2, Application US/09677682

Sequence 2, Application US/09677682

Sequence 2, Application US/09677682

SERERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification

TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification

FILE REFERENCE: 35718/204101 (5718-1118)

GURRENT APPLICATION NUMBER: US/09/677,682
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                                                                                                     ; NAME/KEY: mlsc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: flavin monooxygenase, fully spliced
US-09-677-488A-2
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APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Detoxification
FILE REFERENCE: 35718/204100
CURRENT APPLICATION NUMBER: US/09/677,488A
CURRENT APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOUTHARE FASISED for Windows Version 4.0
          Methods
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                                                                                  TYPE: DNA ORGANISM: Exophiala spinifera FEATURE:
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Matches 1638; Conservative
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APPLICANT: DAMAGOX, JOYCE
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Clasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Decoxification
FILE REFERENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,682A
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
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                                                                                               OTHER INFORMATION: flavin monooxygenase, fully spliced cDNA
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Best Local Similarity 106.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches
  2000-10-02
ER: 09/351,224
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/331
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1638
TYPE: DNA
ORGANIEM: Exophiala spinifera
                                                                                                          US-09-677-682-2
                                                                                        FEATURE:
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APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Colliam, Cacob
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,6828
PRIOR APPLICATION NUMBER: 2000-10-02
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                                                                         NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: flavin monooxygenase, fully spliced
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Pred. No. 0;
0; Mismatches
        NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local Similarity 100.0%;
Matches 1638; Conservative 0
                                               TYPE: DNA
ORGANISM: Exophiala spinifera
DATE: 1999-07-12
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LENGTH: 16
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GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Duvick, Joyce
APPLICANT: Maddox, Joyce
APPLICANT: Maddox, Joyce
APPLICANT: Folkerts, Otto
TITLE OF INVERTION: Compositions and Methods for Fumonisin
TITLE OF INVERTION: Compositions of TITLE OF INVERTION: Detoxification
FILE REPERBNCE: 35718/208255
CURRENT APPLICATION NUMBER: US/09/882,694
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 09/351,224
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches
                 4.0
                  Version
                                          TYPE: DNA
ORGANISM: Exophiala spinifera
FEATURE:
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASLSEQ for Windows
SEQ ID NO 2
                                                                NAME/KEY: misc_feature
                                 LENGTH: 1638
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GENERAL INFORMATION:
APPLICANT: DUVICK, JON
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Compositions and Methods for CURRENT SPPLICATION NUMBER: US/09/882,694A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/351,224
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                                                                               ; LOCATION: (0)...(0)
; OTHER INFORMATION: flavin monooxygenase, fully spliced US-09-882-694.
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                                                                                                                         100.0%; Score 1638;
100.0%; Pred. No. 0;
iive 0; Mismatches
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1638
                                           TYPE: DNA
ORGANISM: Exophiala spinifera
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                                                                      NAME/KEY: misc_feature
LOCATION: (0)...(0)
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GENERAL INFORMATION:
APPLICANT: DUVICK, JON
TILE OF INFUNION: Compositions and Methods for
FILE REPERRORS: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFURNE: PATENTIN Ver. 2.0
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ORGANISM: Exophiala spinifera
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Pred. No. 0;
; Mismatches
                                            : NAME/KEY: misc_feature
: LOCATION: (0)
: OTHER INFORMATION: flavin monooxygenase,
US-09-882-694A-2
PRIOR FILING DAVE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1638
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Best Local Similarity 100.0%;
Matches 1638; Conservative 0;
                               TYPE: DNA
ORGANISM: Exophiala spinifera
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TYPE: DNA
ORGANISM: Exophiala spinifera
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                       Score 1575; D
Pred. No. 0;
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; FEATURE:
; OTHER INFORMATION: flavin
US-09-351-224-1
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Matches 1638; Conserv
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Sequence 1, Application US/09351224E
SEGUERAL INFORMATION:
APPLICANT: DUVICK, JON
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: FOlkerts, Otto
TITLE OF INVENTION: Compositions and Methods;
TITLE OF INVENTION: Compositions and Methods;
TITLE OF INVENTION: Detaxification
FILLE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351, 224E
CURRENT FILLING DATE: 1999-07-12
NUMBER OF SED ID NOS: 11
SOFTWARE: FastSED for Windows Version 4.0
SED ID NO!
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Sequence 1, Application US/09351823
Sequence 1, Application US/09351823
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for Furmonisin Detoxification
TITLE OF INVENTION: Compositions and Methods for Furmonisin Detoxification
TITLE OF INVENTION: US/09/351,823
CURRENT APPLICATION NUMBER: US/09/351,823
CURRENT FILING DATE: 1999-07-12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Exophiala spinifera
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                                                   Score 1575;
Pred. No. 0;
               ; LOCATION: (0)...(0)
; OTHER INFORMATION: flavin monooxygenase
US-09-351-224E-1
                                                   Query Match
Best Local Similarity 96.9%;
Matches 1638; Conservative
        misc_feature
FEATURE:
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Score 1575; DE
Pred. No. 0;
0; Mismatches
        o;
96.2%;
        Matches 1638; Conservative
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Sequence 1, Application US/09677488

GENERAL INFORMATION

TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification

FILLE REPRENCE: 35718/20100 (5778-111A)

CURRENT APPLICATION NUMBER: US/09/677,488

CURRENT FILLNG DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/351,224

PRIOR APPLICATION NUMBER: 09/351,224

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 1
                                                              1200
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ORGANISM: Exophiala spinifera
FEATURE:
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Length 1691;

DB 26;

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Score

28:

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                        53;
              Length 1691;
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              26;
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Pred. No. 0;
0; Mismatches
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             96.2%;
larity 96.9%;
Conservative
                   Similarity
                   Local Sim
les 1638;
US-09-677-488A-1
              Query Match
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APPLICANT: GUESDON, Jean-Luc
APPLICANT: THIERRY, Dominique
APPLICANT: VINCENT, VETONIQUE
APPLICANT: VINCENT, VETONIQUE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH HYBRIDIZE
TITLE OF INVENTION: SPECIFICALLY WITH BACTERIAL STRAINS OF THE MYCOBACTERIUM
TITLE OF INVENTION: AVIOM-INTRACELLULAR COMPLEX
CORRESPONDENCES: 66
CORRESPONDENCE ADDRESS:
Sequence 4, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 19, Appli
Sequence 19, Appli
Sequence 193, Appli
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ADDRESSEE:
BULDS, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandia
STATE: Viginia
CITY: Alexandia
STATE: Viginia
COUNTRY: United States
LIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/08/232,015
FILING DATE: 13-MAY-1994
CLASSIPICATION NUMBER: W0 93/09251
FILING DATE: 13-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/13504
APPLICATION NUMBER: FR 91/13504
APPLICATION NUMBER: 36,113
REPERBENCE/COCKET NUMBER: 36,113
REMOTH: 1642 base pairs
TYPE: NUMBER: SINGLE
US-08-764-233A-4

US-08-47-35A-6

US-08-028-934-6

US-08-028-934-6

US-08-76-233A-1

US-08-716-942-16

US-08-715-946-1

US-09-773-816-1

US-09-98-1

US-08-997-1

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US-08-232-015-2

/ Sequence 2, Application US/08232015

/ Patent No. 5650272

/ GENERAL INFORMATION:
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MOLECULE TYPE: CDI
HYPOTHETICAL: NO
ANTI-SENSE: NO
      April 26, 2002, 19:25:11 ; Search time 150.7 Seconds (Without alignments) 2669.859 Million cell updates/sec
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Sequence 1, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 6, Appli
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-030-99-51-1

US-08-808-321-7

US-08-808-323-7

US-09-102-408-7

US-09-102-408-7

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US-09-103-108-1

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Listing first 45 summaries
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                                                                                Indels 30;
                                                           Length 1642;
                                                        Score 119; DB 1; L. Pred. No. 1.5e-25; 0; Mismatches 600;
             Mycobacterium avlum
                                                       Query Match
Best Local Similarity 48.3%;
Matches 589; Conservative
) ORIGINAL SOURCE:

) ORGANISM: MyC

US-08-232-015-2
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OTHER INFORMATION: "A" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                 1071 agaacaatcgcccattgtggctgttacaaaqacaggtgtgctcttgagtgacggcagcaa 1130
1435 CCGCAAGACGCCGATCATCCATCGACGGACGGCATTAAACACGACGG---CCCA 1491
                                                                                                                                                                                                                                      gagggaatgcgacacgatcgtgctggcgacgggtttcgacagtttcactggctcattgac 1190
cocactggagagagactactacgaaatgctggacaagccgagcgtcgaaattgtgaatct 1070
                                  1492 TTACGACCTCGACGCGATCGTGGCGACCGGATTCGACGCGATGACCGGCGCGCTGGC 1551
                                                                                                                                                                                                                                                                                                                                                               acatatgggcttgaaaaacaagcacggagtggacctgaaggaggtgtggaaagatggcat 1250
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APPLICANT: WHITE, Owen R.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: PEASE. Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFWARE: PETENTIN VET. 2.1
LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1612 CCGCACGTACCTGGGCCTC 1630
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1569226 ggacccggggggggggaarcacagccaggrrccrgarcagcgcargcggcarrcrgacggr 1569167
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APPLICANT: Wang, Yongzhao.
APPLICANT: Childs, John D.
APPLICANT: Childs, John D.
APPLICANT: Childs, John D.
APPLICANT: Childs, John D.
APPLICANT: Squires, Charles H.
TITLE OF INVENTION: A Gene Involved in Thiophene
TITLE OF INVENTION: A Gene Involved in Thiophene
FILE REFERENCE: EBC97-05
CURRENT APPLICATION NOWBER: US/09/030, 995
CURRENT PILING DATE: 1998-02-26
SOFTWARE: FESTERQ for Windows Version 3.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 groggotggccatgttgcgacggcaaagtatctcattctcgctacggggttgctccacag 455
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Patent No. 5767373
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     gccagagagtcgccgtcatcggtgccgg 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: No. 6235519ardia asteroides
US-09-030-995-1
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US-09-030-995-1
Sequence 1, Application US/09030995
Patent No. 6235519
GENERAL INFORMATION:
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US-08-472-028A-7
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Best Local S:
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1569125 GAACACCAAGGTGGTCGCCGAGTTCGATGACGAGCACCAGGCCGGGTGCAAAC 1569066
                                                                                             1569065 GGACCCGGGGGGGGGAATCACAGCTGCTGATCAGGGCATTCTGACGGT 1569006
                                                                                                                                                                                      Db 1569005 GCCCAAACTACCCGACATCGACGGGGTGGACTCGTTTGAAGGCGTCACCATGCACACGC 1568946
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                                                                396 gtcggctggccatgttgcgacggcaaagtatctcattctcgctacggggttgctccacag 455
                                                                                                                                                  gegaaageteagaeteaaegeeaaatettegaaggaageeeeegattttggeggegt--- 155
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TITLE OF INVERTION: TUBERCULOSIS
FILE REFERENCE: 24365-20007.00
CURRENT APPLICATION NUMBER: US/O9/103,840A
KUNNER OF SEQ ID NOS: 2
SOFWARE: PATENTIN VOS: 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 1568825 GCGCACCCCTATTGGTGTTTCCCCA 1568800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGATISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                        636 gcgaaggccgagctattgtctgccca 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLEISCHMAN, Robert D.
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US-09-103-840A-1/c
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21P: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 7, Application US/08B0B931

Patent No. 5939602

GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Volrath, Sandra
APPLICANT: Ward, Eric
APPLICANT: No. 5939602artis Corporation
STRRET: 520 White Plains Road, P.O. Box 2005
CITT: Tarytown

STRRET: APPLICANT

STRETT: APPLICANT

STRRET: APPLICANT

STRRET: APPLICANT

STRRET: APP
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2.1%: Score 34.4; DB 1; Length 2061;
Best Local Similarity 59.0%; Pred. No. 1.9;
Matches 59; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,028A
FILING DATE:
CLASSIFICATION WIMBER: 36,129
NAME: Elmert James Socott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
TELECOMMUTICATION INFORMATION:
TELEFAX: 919-541-8614
TELEFAX: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: OUCLAIC ACID
STRANDEDNESS: SINGLE
THERET STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
) LOCATION: 64..1698
; OTHER INFORMATION: /note= "Maize protox-2 cDNA;
) OTHER INFORMATION: sequence from pWDC-3"
US-08-472-028A-7
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Cor
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE: NO
                                                                                                                                                                                                                       USA
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-08-808-931-7
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08608323
; Patent No. 6018105
; Patent No. 6018105
; Patent No. 6018105
; Patent No. 6018105
; Patent No. 1040800, Marie
; APPLICANT: Volleath, Sandra
; APPLICANT: Volleath, Sandra
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: Promoters from Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
; NUMBER OF SEQUENCES: 26
; CORRESCONDENCE ADDRESS:
; ADDRESSEE: No. 6018105artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 gegaaageteagaeteaaegeeaaaatettegagggagee 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . LOCATION: 64.1698

COPHER INFORMATION: /product "Maize protox-2"

US-08-808-931-7
                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08 60/012,705
FILING DATE: 28 FEB-196
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28 FEB-196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
ATTORNEY AGENT INFORMATION:
NAME: Melgs, J. Timchy
REGISTAATION NUMBER: GC 1847
RECISTAATION NUMBER: GC 1847
RECISTAATION NUMBER: GC 1847
RECISTAATION NUMBER: GC 1847
TELECOMMUNICATION INFORMATION:
TELEFAX: (919) 541-8689
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TTPE: NUCLEIC acid
STRANDEDNESS: SINGIE
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
CRIGINAL SOURCE:
GROANISM: Zea mays (maize)
IMMEDIATE SOURCE:
CLONE: PWDC-3 (NRRL B-21259)
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Ouery Match 2.1%; Score 34.4; DB 3; Length 2061; Best Local Similarity 59.0%; Pred. No. 1.9; Matches 59; Conservative 0; Mismatches 41; Indels 0
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CCUNTRY: USA
ZIP: ACCOUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPALIBLE
CASIFICATION NUMBER: US 08/08,931
FILING DATE: 28-FEB-1996
FILING DATE: 21-UN-1996
FILING DATE: 21-UN-1996
FILING DATE: Z1-UN-1996
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LOCATION: 64..1698

COTHER INFORMATION: /product- "Maize protox-2"
US-09-050-6038-7
      INVENTION: Protoporphyrinogen Oxidase SEQUENCES: 37
TITLE OF INVENTION: Protoporphytungen communication SEQUENCES: 37 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 6023012artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLIC...
FILING DATE: L. ATTORKEY ACENT INFORMATIC...
NAME: MAIGH, J. TINGCHY
REGISTRATION NUMBER: 38,741
REFERENCE/DOCKET NUMBER: CGC 1847
TELEPHONE: (919) 541-8587
TELEPHONE: (919) 541-8689
INFORMATION: (919) 541-8689
INFORMATION: (910) 541-8689
INFORMATION: (910) 541-8689
INFORMATION: (910) 541-8689
INFORMATION: 2001 D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-102-420B-7
; Sequence 7, Application US/09102420B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays (maize)
IMMEDIATE SOURCE:
CLONE: DWDC-3 (NRRL B-21259)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-CENTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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US-09-050-603A-7
: Sequence 7, Application US/09050603A
: Patent No. 6023012
: GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
: APPLICANT: Obnison, Marie
APPLICANT: Potter, Sharon
APPLICANT: Petter, Sharon
APPLICANT: Heifetz, Peter
: APPLICANT: Heifetz, Peter
: TITLE OF INVENTION: DNA MOLECULES Encoding Plant
                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Inh PC compatible
COMPUTER: Inh PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PAREITER Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/808,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 gogaaageteagaeteaacgeeaaatettegagggagee 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ). LOCATION: 64..1698
; OTHER INFORMATION: /product- "Maize protox-2"
US-08-808-323-7
                                                                                                                                                                                                                                                                                            CLASSIPLCATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 60/012,705
FILING DATE: 28-FEB-1996
APPLICATION UNBER: US 60/013,612
FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
FILING DATE: 28-FEB-1996
APPLICATION UNBER: US 60/020,003
FILING DATE: 21-1949-1996
ATTORNEY/AGENT INFORMATION:
NAME: Medis, J. Timothy
REGISTRATION NUMBER: 38,241
REFERNCE/DOCKET UNBER: 36,241
FELEFAU. (919) 541-8699
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LERGAT: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays (maize)
IMMEDIATE SOURCE:
CLONE: PWDC-3 (NRRL B-21259)
                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
         Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Zea n
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CITY: Ta
STATE: N
COUNTRY:
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GENERAL INFORMATION:
APPLICANT: VOLATE, Sandra
APPLICANT: Ward, ETC.
APPLICANT: Ward, ETC.
APPLICANT: Ward, ETC.
APPLICANT: Ward, ETC.
CORRESPONDENCE ADDRESS: 43
CORRESPONDENCE ADDRESS: 43
CORRESPONDENCE ADDRESS: 43
CORRESPONDENCE ADDRESS: 43
COMPUTER REALABLE FORM:
COUNTY: NO.
COUNTY: NO.
COUNTY: NO.
COMPUTER: ELADRA 41x
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LOCATION: 64..1698
OTHER INFORMATION: /product= "Maize protox-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWDC-3 (NRRL B-21259)
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2061 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                        RESULT 10

105-09-071-296-7

Sequence 7, Application US/09071296

Patent No. 617745

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ward, Eric R

APPLICANT: Volrath, Sandra

TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                       Gaps
                                                                                                                                                               39 cgcatgcgacgccatcatcgttggagccggcctcagcggcatctctgctgtgtacaaatt 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                  Score 34.4; DB 3; Length 2061;
Pred. No. 1.9;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

2.1%; Score 34.4; DB 4; Length 2061;
Best Local Similarity 59.0%; Pred. No. 1.9;
Matches 59; Conservative 0; Mismatches 41; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA: US/09/071,296
FILING DATE: 06-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Malze protox-2 cDNA; sequence from pWDC-3"
                                                                                                                                                                                                                                                              99 gogaaagotcagactcaacgocaaaatottogagggagoc 138
                                                                                                                                                                                                                                                                                         255 CAGACAGAGCGGCGTGAACGTAACGGTGTTCGAAGCGGCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-UN-94
ATTORNEY/ACENT INFORMATION:
NAME: EIMER: James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GCC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELERATION FOR SEC 10 NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 Dase pairs
TYPE: NUCLEIC acid
TYPE: ALCIELC acid
TYPE: ALCIELC acid
TYPE: ALCIELC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                    Query Match 2.1%;
Best Local Similarity 59.0%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUTCOMEST TABEST MODECULE TYPE: CDNA HYPOTETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAME/KEY: CDS
CCATION: 64.1698
OTHER INFORMATION:
OTHER INFORMATION:
US-09-071-296-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-09-102-420B-7
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Sequence 7, Application US/09015683
Sequence 7, Application US/09015683
Patent No. 6288306
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wolf and the APPLICANT: Volrath, Sandra
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Clas-Gelgy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 34.4; DB 4; Length 2061; 59.0%; Pred. No. 1.9; tive 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09191998
Fatent No. 6307129
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 64.1698
COTHER INFORMATION: Anote-"Malze protox-2 cDNA;
COTHER INFORMATION: sequence from pWDC-3"
CS-09-015-683-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZOMENTER PREABABLE FORM:
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 CAGACAGAGCGGCGTGAACGGTGTTCGAAGCGGCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 gogaaagotcagactcaacgocaaaatcttcgagggagcc 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Blimer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-541-8689
INPORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 59.0%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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US-09-191-998-7
                                                                                                                                                                              US-09-015-683-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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39 egcatgcgacgccatcatcgttggagccggcctcagcggcatctcgctgtgtacaaatt 98 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 [1] 1 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09196268
Patent No. 6282837
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
APPLICANT: STREET: Stribardenisms
CORRESPONDENCE ADDRESS: STRIBARD: STREET: STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 cgcatgcgacgccatcatcgttggagccggcctcagcggcatctctgctgtgtacaaatt 98
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2.18; Score 34.4; DB 4; Length 2061;
Best Local Similarity 59.08; Pred. No. 1.9;
Matches 59; Conservative 0; Mismatches 41; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY:
COMPUTER READABLE FORM:
MEDIUM TYPE:
FIEDRY SYSTEM:
PC-DOS/MS-DOS,
SOFTWARE:
FILON SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
FILING DATE:
FILING SOFTHATION:
FILING SOFTHATION:
FREFERENCE/COCKET NUMBER:
FILING DATE:
FILING DA
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OTHER INFORMATION: Sequence from pWDC-3"
CPHER INFORMATION: sequence from pWDC-3"
                                                                                                                                                                                                                                    99 gogaaageteagaeteaaegeeaaaatettegagggagee 138
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                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/497,698
FILING DATE: 03-Reb-2000
CLASSIFICATION: <unknown>
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: CTHER INFORMATION: /Product- "Maize protox-2"
: SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATE:

FILING DATE: CURRICON
FILING DATE: COF, CURRICON
FILING DATE: CURRICON
FILING
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Query Match

Best Local Similarity 59.0%; Pred. NO. 1.9;

Matches 59; Conservative 0; Mismatches 41;
   : Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1998
11-MAR-1998
28-FEB-1996
28-FEB-1996
21-30N-1996
06-JUN-1995
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IMMEDIATE SOURCE:
CLONE: PWDC-3 (NRRL B-21259)
                                                            COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Johnson, Marie-
Ward, Etic
Halfetz, Peter
HITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSE: No. 6308458artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%; Score 34.4; DB 4; Length 2061; Best Local Similarity 59.0%; Pred. No. 1.9; Matches 59; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 64..1698
CTHER INFORMATION: /note- "Maize protox-2 cDNA;
CTHER INFORMATION: sequence from PWDC-3"
US-09-191-998-7
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,998
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 gegaaageteagaeteaaegeeaaaatettegagggagee 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELENO JUATE: UO-JUN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGRAT INFORMATION:
NAME: Elner, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/POCKET NUMBER: GGC 1748/CIP
TELEPAN: 919-541-669
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNISS: single
TOPOLIGY: linear
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
TITLE OF INVENTION: Oxidase Enzyme NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-03-43/10-09
Sequence 7, Application US/09497698
Patent No. 6308459
GENERAL INPORMATION:
APPLICANT: Volrath, Sandra
Johnson, Marie
                                                                                                                             STREET: 7 Skyllr
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-497-698-7
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                                                                         RESULT 15
Us-09-265-108-1
Sequence 1. Application US/09265108
Sequence 1. Application Numberly
TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
TITLE OF INVENTION: Having Cellobiose Dehydrogenase Activity
FILE REFERENCE: 5850.000-US
CURRENT APPLICATION NUMBER: US/09/265,108
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2576
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.1%; Score 34; DB 3; Length 2576;
Best Local Similarity 52.9%; Pred. No. 2.8;
Matches 73; Conservative 0; Mismatches 65; Indels
Search completed: April 27, 2002, 00:19:28 Job time: 17657 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Humicola
US-09-265-108-1
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2. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

3. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

5. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

5. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

5. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

7. $IDSI, gegdata/hold-geneseq/geneseqn-embl/MA1981.DAT:*

8. $IDSI, gegdata/hold-geneseqy/geneseqn-embl/MA1981.DAT:*

8. $IDSI, gegdata/hold-geneseqy/geneseqn-embl/MA1981.DAT:*

8. $IDSI, gegdata/hold-geneseqy/geneseqn-embl/MA1981.DAT:*

10. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

11. $IDSI, gegdata/hold-geneseqy/geneseqn-embl/MA1991.DAT:*

12. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

13. $IDSI, gegdata/hold-geneseqy-embl/MA1991.DAT:*

14. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

15. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

16. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

17. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1991.DAT:*

21. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1999.DAT:*

22. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1999.DAT:*

23. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1999.DAT:*

23. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1999.DAT:*

23. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA1999.DAT:*

24. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA2001B.DAT:*

24. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA2001B.DAT:*

24. $IDSI, gegdata/hold-geneseqy-geneseqn-embl/MA2001B.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

		Description	10111111111111111111111111111111111111	TOTAL DEPTH OF THE PARTY OF THE	Exophiala spinifer	Aspergillus oryzae	Mycobacterium avíu	Aspergillus oryzae	Mycobacterium tube	Mycobacterium tube	R. ruber cddA gene	R. ruber 10kb gene
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ט כ		8. 6.	2.6	536165	16	AAV30459	Rhizobium species
)	12	4 1 4			23	AAS59593	Propionibacterium
	3.	40.2		1677	21	AAZ91256	Flavin monooxygena
	14	40.2		24494	21	AA291253	Bacterium 2412.1 f
	15	37.6		747	22	AAH76382	Nucleotide sequenc
	16	37.6		1365	20	AA221172	N, asteroides stra
	17	37.6		1812	22	AAH22890	R, ruber cyclodode
	18	36.8		362	21	AAA31587	rosatell
	19	36.6		733	21	AAC66233	Human Mad3 gene se
	20	35.6		1812	22	AAH22888	R, ruber cyclodode
	21	35.4		4590	22	AAH24065	Yeast AOD9604-asso
	22	35.2		536	21	AAZ91289	Fumonisin-cataboli
U	23	35		2132	23	AAS68025	DNA encoding novel
U	24	34.8		1769	23	ABL12489	Drosophila melanog
U	25	34.8		3769	23	ABL12488	Drosophila melanog
U	56	34.8		6077	23	ABL12266	Drosophila melanog
	27	34.4		265	21	AAC10532	Human secreted pro
	28	34.4		356	21	AAA31895	
	53	34.4		2051	22	AAD15430	Maize protoporphyr
	30	34.4		2061	17	AAT11676	
	31	34.4	•	2061	18	AAV04307	
	32	34.4		2061	18	AAT86131	
	33	34.4		2061	19	AAV07254	
	34	34.4		2061	22	AAD21860	
	35	34.4		2061	22	AAF76574	Maize protoporphyr
	36		•	2061	22	AAD17334	Maize protoporphyr
	37	34		435	21	AAF08106	venenat
	38	34	•	2576	21	AAZ95701	Humicola insolens
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RES	RESULT	1					
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Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permesse; pelyrooptorein; fumonisin esterase; detoxification; mycotoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
                                                                                                                                  Exophiala spinifera flavin monooxygenase coding sequence.
                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                               99WO-US15824
                                                                                                                                                                                                                            99WO-US15824
                          02-MAY-2001 (first entry)
                                                                                                                  Exophiala spinifera.
                                                                                                                                                                                     WC200105980-A1.
                                                                                                                                                                                                                           14-JUL-1999;
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                                                                                                                                                                                                        25-JAN-2001.
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AAD02691 standard; DNA; 1638 BP.

AAD02691;

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The patent discloses novel polynuclectides encoding Exophiala spinifera funchisin degradative or transport enzymes such as flavin monocoxygenase. Eldehyde dehydrogenase, permease and pajvoprotein. A kumonisin esterase erzyme with at least one fumonisin degradative enzyme is useful for erzyme with at least one fumonisin degradative enzyme is useful for decoxifying fumonisin or a structurally related mycotoxin present in harvested grain, on application to a plant or to harvested grain or a structurally related mycotoxin present in harvested grain, or to processed grain that is to be used as animal corrected or muman feed, or as a silage. Nuclectide fragments of the present in twention are useful as probes and primers. They can be introduced into microorganisms that multiply on plants to deliver enzymes to conclude a vector into a microbial host and the degrading enzymes are introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the invention are fermented in a bacterial host and the resulting bacteria is processed and used as a microbial spray. The nucleotide sequences is present an example fumonish and resist its toxic effects.

C The present DNA sequence is the flavin monoxygenase coding sequence
                                                                                                               Novel polynucleotides encoding Exophiala degradative or transport relayme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food consumption
                    OR;
                    Crasta
                    ò
                    Folkerts
                    J,
                                                                                                                                                                                                                                                    English.
                    Gilliam
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                                                                                                                                                                                                                                            Claim 1b; Page 64; 90pp;
                    Maddox J,
                                                              WPI; 2001-147345/15.
P-PSDB; AAY72634.
                  Duvick JP,
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ö 240 tggacctggtcttgccgctatcctgaccagaaagagttgctgtcatatgttcaccactgt 300 360 ggagccggcctcagcggcatctctgctgtgtacaaattgcgaaagctcagactcaacgcc 120 ggagccggcctcagcggcatctctgctgtacaaattgcgaaagctcagactcaacgcc 120 aaaatcttcgagggagcccccgattttggcggcgtctggcactggaaccgctaccctggc 180 tggacctggtcttgccgctatcctgaccagaaagagttgctgtcatatgttcaccactgt 300 Gaps getegtgttgatteggagaegecettetaceaaetgaacatteecagaagtatggaaagae Length 1638; ö Indels Ouery Match 100.0%; Score 1638; DB 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches 0; I 241 61 61 121 121 181 241 181 301 301 361 361 421 421 q q ö g δ a ò g õ ò q ŏ õ g ò

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T; 0 other;

Sequence 1638 BP; 388 A; 432 C; 462 G; 356

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function degradative or transport enzymes such as flavin monoxygenase, aldenoisin degradative or transport enzymes such as flavin monoxygenase, aldenyde dehydrogenase, permease and progredein. A fumonisin esterase aldehyde dehydrogenase, permease and progredein. A fumonisin esterase enzyme with at least one fumonisin degradative enzyme is useful for detoxifying fumonisin or a structurally related mycocoxin present in detoxifying fumonisin or a structurally related mycocoxin present in harvested grain, on application to a plant or to harvested grain or harvested grain, on application to a plant or to harvested grain or a silage. Nucleotide fragments of the present or human feed, or as a silage. Nucleotide fragments of the present into microcorganisms that multiply on plants to deliver enzymes are introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the proposition or a fermented in a bacterial host and the resulting bacteria is parcessed and used alone or in combination to engineer microbes or other or present sequence is a genomic DNA encoding szophiala spinifera or the present sequence is a fumonisin degradative enzyme.
Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; addahyde dehydrogenase; permease; p-tyvcorcheth; tumonisin esterase; detoxification; mycoccoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
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                                                                                                                                                                                                                                                                                                                   Exophiala spinifera flavin monooxygenase genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1b; Page 63-64; 90pp; English.
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P-PSDB; AAY72634.
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                     Clausen IG,
                                                                                                                                                                                                                                                                           Sequence 695 BP; 162 A; 175 C; 190 G; 166 T; 2 other;
                      Rey MW, Shuster JR, Kauppinen S,
                                                                            Claim 88; Page 2091; 3161pp; English.
) NOVO NORDISK BIOTECH INC.
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                      Berka RM,
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Recombinant cosmids were packaged in vitro and used to transform E.coli HB101. DNA was isolated from positive colonies and the Sali fragments were tested for hybridisation with M.avium.

M.intracellulare and M.tuberculosis H37v. Cosmid clone I-6 (AAQ41978) hybridised to M.avium only; clone I-1 (AAQ41979) hybridised with DNA from both M.avium and M.intracellulare. I-6 and I-1 have been cloned in pucies to produce plasmids pM01 (CNCM I-1138), respectively. The invention also covers oligonic leaders and primers derived from the sequences of I-6 and
ocogoactcoccggoctcgccgattcaacgggaaggtgattcattcgagtgcctggcac 525
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                                                                                                                                                                                                                                                                         Polymerase Chain Reaction; PCR; acquired immune deficiency syndrome; Johne Disease; mycobacteria; M.a-i complex; detection; ss.
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of e.g.
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48.3%; Pred. No. 2.9e-26;
ive 0; Mismatches 600; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences specific to Mycobacterium avium-intracellulare - and derived probes and primers, for specific diagnosis opportunistic infection in AIDS patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1642 BP; 283 A; 564 C; 541 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vincent V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 22-24; 74pp; French.
                                                                                                                                                            BP
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                                                                                                                                                         AAQ41978 standard; DNA; 1642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                                                                                                                  Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Tichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
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                                                                                                                                                                          Aspergillus oryzae EST SEQ ID NO:4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 88; Page 1928; 3161pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rey MW, Shuster JR,
                                               BP.
                                           AAF12000 standard; cDNA; 702
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                                                                                                                                 (first entry)
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Gaps

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Query Match
4.9%; Score 80.8; DB 21; Length 702;
Best Local Similarity 46.6%; Pred. No. 1.5e-14;
Matches 293; Conservative 0; Mismatches 333; Indels 3

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caatacctccgggacgtggtggaagataccactccgcaaacacatgcagttcaacacc 317
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                                  18 gatgocottgiogiatgigooggottiggiggaattiataogototattocottgioaag
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ID AA199683 standard; DNA; 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1569416 CGACTACCACGCACTGATCGTCGCGCCGGGTTCTCCGGGGATCGGCGCCGCAATCAAGCT 1569357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1569356 CGACCGGGCGGGATTCACCGACTACCTCGTGGTCGAAGCCGGGGACGGTGTCGGCGGGAC 1569297
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                                                                                                                                                                                                                                                                           The invention relates to evaluating strain variation within and between different populations of the tubercollosis bacterial pathogen. Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (An199683) and H37Rv (AA199681). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of the tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monitoring.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=629432881.
Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Ry differ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                    Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
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Db 1569577 CGACTACCACGCACTGATCGTCGGCGCCGGGTTCTCCGGGGATCGGCGCGCAATCAAGCT 1569518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID~6294328B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Wycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the first strain at positions in the complete sequence of the more partial at positions in the discoundable of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA19968) and H37Rv (AA199682). The method is useful for evaluating strain variation of tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 ctggcactggaaccgctaccctggcgctcgtgttgattcggaagacgcccttctaccaact 215
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                                                                                                                                                                                                                                       Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemic monitoring; ds.
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3.3%; Score 53.8; DB 22; Length 4411529;
Best Local Similarity 49.0%; Pred, No. 000049;
Matches 307; Conservative 0; Mismatches 307; Indels 12; GS
                                                                                                                                                                                            Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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2.8%; Score 46.6; DB 22; Length 1812;
Best Local Similarity 45.7%; Pred, No. 0.0012;
Matches 206; Conservative 0; Mismatches 239; Indels 6;
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 Claim 8; Page 51; 78pp; English.
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                                                 Db 1569046 CTCGGCGGTGCAGGTCATTCCGAGATGCGCCCAATTGTCTCCCACCTTTTTCA 1568987
....-CTCTTTCGAGCAGAGCGGCACTGGTCGCGCACCTATGCACCGGACACGA 1569347
                                                                                                                                                                                                                                               1569166 GCCCAAACTACCCGACATCGACGGGGTGGACTCGTTTGAAGGCGTCACCATGCACACCGC 1569107
                                                                                                                                                                                                                                                                                                           1569106 ACGCTGGGATCACACCCAGGACCTGACCGGCAAGCGCGTCGGGATCATCGGCACCGGGGC 1569047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclododecanone; degradation; lauryl lactone esterase; cddA; cddB; cdd: dddecanolc dlac4d; cyclododecanone monoxygenase; cyclic ketone; cddY; 12-hydroxylauric acid dehydrogenase; 12-oxy lauric acid dehydrogenase; nacrolactone; microbiological; cddC; cddD; ds.
                                                                                                                                                                                                                                                                          516 tgcctggcacgaagacttcgacgcagaggccagagatcgccgtcatcggtgccggggc 575
                                                                                                                                                                                                                 Isolated nucleic acids encoding dodecanoic diacid synthesizing enzyme, extboddecanone monoxygenase for bioproduction of dodecanoic diacid from cyclododecanone .
                              276 gttgctgtcatatgttcaccactgtgacaagatccgggggcttgagaaaagacgtctactt 335
                                                                                          336 cggagctgaggtggttgatgcgcggtatgccagagatctgggcacctggactgtcaagac 395
                                                                                                                                                      396 groggetagecatgitgegaeggeaaagtateteattetegetaeggggttgetecaeag 455
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1..1812
Agene cddA forcanone monooxygenase //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH22871 standard; DNA; 1812 BP
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P-PSDB; AAB85234.
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Db 1569397
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1202 eccgggategaategtteegeggeaagtegtteeacaeceagtegatgggaetaegaetae 1261
                                                                              1082 ctggtctggcaggagcacgatcagcgctggcggatctcgacgaaccgaggtgaccacttc 1141
                                                                                                                                                           1142 acggeceaattegtgggtatgggeaceggeectetgeacgtggegeagetgeegggeate 1201
1022 cgaatcggcaaacactacgacttgtacgacgacgcgctgttccacaccgaagtcaccgac 1081
                                      355 gegeggtatgecagagatetgggeacetggaetgteaagaegteggetggceatgttgeg 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dehydrogenase-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation; legume; plant; ds.
                                                                                                                                                                                                   ocogoctogocgatttoaaogggaaggtgattcattogagtgcctggcacgaagacttc
                                                                                                                         acggcaaagtatctcattctcgctacggggttgctccacaggaagcacactcccgcactc
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/product= "aminotransferase-like prof
/note= "homologous to the BioA gene"
424056.,425594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "homologous to the OppC gene" 418631.419680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "ORF K2"
product "oligopeptide permease"
/note= "homologous to the OppD gene"
419677..420738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note- "homologous to the CapA gene' 22628..424031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tnp gene"
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/note= "homologous to the Tnp gen
428292..429623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF K4"
/product= "encapsulation-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF K6"
/product= "(semi)aldehyde d
complement (426949,.428028)
                                                                                                                                                                                                                                                                                                                        1262 accggcggcgacgcgctgggcgcgccgatgg 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF K1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "ORF K7"
                                                                                                                                                                                                                                                                                    535 gacgcagagggccagagagtcgccgtcatcg 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ORF K3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "ORF K8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "ORF K3"
/product= "oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
417796..418671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium species plasmid pNGR234a.
                                                                                                                                                                                                                                                                                                                                                                                                            )458/c
AAV30458 standard; DNA; 534720 BP
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/standard_name=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to genes from Rhodococcus ruber involved in cyclododecanone degradation pathway. A 10 kb cluster from R. ruber was cyclododecanone degradation pathway. A 10 kb cluster from R. ruber was related that comprises genes (designated cdda, cddb, cddy, cddy, cddr, cddb) encoding enzymes such as dodecanoid synthesizing enzyme, cyclododecanone monocoxygenase, lauryl lactone esterase, 12-hydroxylauric acid dehydrogenase, Host cells comprising the nucleic acids are used for the production of dodecanedioic acid when contacted with cyclododecanone, lauryl lactone when contacted with cyclododecanone, 12-hydroxy lauric acid when contacted with 12-hydroxy lauryl acid when contacted with 12-hydroxy lauric acid when contacted with 12-hydroxy lauric acid when contacted with 12-cox lauric acid. They are also useful for the production of hydroxy acids when contacted with cyclodocanone, c
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                      Cyclododecanone; degradation; lauryl lactone esterase; cddA; cddB; cddX; dodecanore, diacid; cyclododecanone monoxygenase; cyclic ketone; cddY; 12-hydrxylauric acid dehydrogenase; 12-oxo lauric acid dehydrogenase; macrolactone; microbiological; cddC; cddD; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               968 tacatgoccaccgaga----agtacgcgcacggcccggagatcctcgaacactgccaa 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids encoding dodecanoic diacid synthesizing enzyme, cyclododecanone monooxygenase for bioproduction of dodecanoic diacid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cactgtgacaagatccggggcttgagaaaagacgtctacttcggaggtggttgat 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 aaagactggacctggtcttgccgctatcctgaccagaaagagttgctgtcatatgttcac 294
                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB85324, AAB85325, AAB85326, AAB85327, AAB85328, AAB85329.
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45.7%; Pred. No. 0.0031;
iive 0; Mismatches 239; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10480 BP; 1928 A; 3471 C; 3366 G; 1715 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                 Chen MW, Cheng Q, Gibson KJ, Kostichka KN, Thomas SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 62-65; 78pp; English.
                                                                                                                                                                                                                                                                                                                        (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                    99US-0170214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from cyclododecanone -
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-451630/48.
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les 206; Conserv
                                                                                                                         Rhodococcus ruber.
                                                                                                                                                             WO200142436-A2.
                                                                                                                                                                                                                                                                                  10-DEC-1999;
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Matches
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/gene= "dctA" /product= "C4 dlcarboxylate transport protein" /note= "homologous to the DctAI gene" 446599447843 /*tag x / ftandard_name= "ORF L1" /product= "cytochrome P450-like protein" /note= "homologous to the Camc gene" /standard_name= "ORF L2" /standard_name= "ORF L2" /product= "gamma-hoxachlorocyclohexane-dechlorinase-like product= "gamma-hoxachlorocyclohexane-dechlorinase-like /note= "homologous to the Lina gene"	ein wit oha-suk e LuxA	/gene"   11D   79   79   79   79   79   79   79   7	blosynthesis"  /note= "homologous to the NifB gene" 457687459096 /*tag= ae /*tandard_name= "ORF L9" /product= "protein involved in FeMo co-factor /note= "homologous to the FixF gene" /\$5093459575 /*tag= af /product= "protein of unknown function" /note= "homologous to the NifX gene"	agout a control of the control of th	nometrogous  1 461845  ct="protein" 1464739  rd_name="ORetions" rd_name="ORetions" 1466079  rd_name="ORetions" rd_name="ORetions" rd_name="ORetions" rd_name="ORetions" rd_name="ORetions" rd_name="ORetions"
CDS	cDS CDS CDS	CDS	CDS	CDS	CDS CDS
/product= "glutamate dehydrogenase-like protein" /note= "homologous to the GLUDI gene" complement (430338431284) /*tag= "transposase homologue" /product= "transposase homologue" complement (431296432840) /*tag= j /standard_name= "ORF K10" /product= "transposase homologue" /note= "homologus to the Tnp gene" /note= "homologus to the Tnp gene" /note= "homologus to the Tnp gene" /*tag= k /*tag= k /*tag= k	T a car a car	/standard_name- "ORF K14" /gene= "nifB" /product= "protein involved in FeMo co-factor complement (436460.438130) /*tag= "ORF K15" /gene= "nifA" /product= "positive regulator of nif, fix and other genes"	complement (438297438590)  /*tag" p /standard_name="ORF K16" /gene="fixx" /product="protein required for nitrogenase activity" /standard_name="ORF K17" /standard_name="ORF K17" /product="protein required for nitrogenase activity" /gene="fixc" /product="protein required for nitrogenase activity" /complement (439923.441032) /*tag="fixc" /standard_name="ORF K18"	/gene="fixb" /product="protein required for nitrogenase activity" /product="protein required for nitrogenase activity" /*tag= s /pene="fixb" /pene="fixb" /product="protein required for nitrogenase activity" /product="protein required for nitrogenase activity" /product="protein required" /product="protein required"/	/standard_name="ore nzo" / product="protein of unknown function" / product="protein of unknown function" / standard_name="ORF K21" / product="protein of unknown function" / standard_name="ORF K22" / standard_name="ORF K22" / standard_name="ORF K22" / standard_name="ORF K22" / product="ferrodoxin-like protein" / note="homologous to the Nifq gene" / standard_name="ORF K23" / standard_name="ORF K23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of the plasmid pNGR234a isolated from halzobium sp. NR234. Open reading frames (ORF) derivable from the nucleotide sequences are claimed. The nucleotide sequences or ORFs can be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences. ORFs or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenobiotic substances in a host organism or the modification of the host range, nitrogen fixation abilities; for obtaining a synthetic minimal set of ORFs required for functional Nizobium-legume symbiosis, especially for nodulation efficiency on host plants.
                                                                                                                                                                                                                                                                        Oy 556 gccgtcatcggggccacaagcatccagattgttcaggagttggccaagaaggt 615 liii i i li li li li li bb 171636 GCCGTGATTGGCAATGGCGCATCGGCAATGCAGGTTGTTCCCGCCATCGCAGGTGTTTTCCCGCAATGGCGGTG 171577
                                                                                                                                                               Db 171756 GCCGTGGGGGGCTTCACCACGCCGAAATGGCCCAACCTTTCGGGCCTGCGCAACTTCGAC 171697
                                                                                                                                                                                                                                   Db 171696 GGCCCGGTGGTGCACACTCGAAATGGGATCCAGAAGTCGCGCTCGACGGTAAACGTGTG 171637
                                                                                                                                                                                                    496 gggaaggtgattcattcgagtgcctggcacgaagacttcgacgcagaggccagagagtc 555
                                                                                                                             436 gctacggggttgctccacaggaagcacactcccgcactccccggcctcgccgatttcaac 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation; legume; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated symblotic plasmid from Rhizobium sp. NGR234 - used to develop products for modifying plant characteristics, e.g. nitrogen fixation, synthesis of compounds and stress response
                                                     Length 534720;
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                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosenthal A;
/note- "homologous to the PP gene"
466590..467021
                                                   Score 41.8; DB 19;
Pred. No. 0.84;
0; Mismatches 97;
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(BIOL-) LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium species symbiotic plasmid pNGR234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV30459 standard; DNA; 536165
                                                                                                                                                                                                                                                                                                                                                                                  Db 171576 GGTGCGTTGACAATCTT 171560
                                                   2.68;
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96EP-0730001.
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                                                                                                                                                                                                                                                                                                                                                  616 gaccaggtaaccatgtt 632
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                                                                                          Conservative
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                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Broughton WJ,
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                                                                                        Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 171696 GGCCCGGTGCTGCACCTCGAAATGGGATCCAGAAGTCGCGCTCGACGGTAAACGTGTG 171637
                                                                                                                                                                                                                                                                                         Db 171756 GCGTGGGGGGCTTCACCACGCCGAAATGGCCCAACCTTTCGGGCCTGCGCAACTTCGAC 171697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                            436 gctacggggttgctccacaggaagcacactcccgcactccccggcctcgccgatttcaac 495
Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful fureating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                             496 gggaaggtgattcattcgagtgcctggcacgaagacttcgacgcagagggccagagatc
                                                                                                   Length 536165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein encoding DNA #88.
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                                                                                                                                                                Indels
                                                                                            Score 41.8; DB 19;
Pred. No. 0.84;
0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS59593 standard; DNA; 10524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 171576 GGTGCGTTGACAATCTT 171560
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                   2.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616 gaccaggtaaccatgtt 632
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                                                                                                                                                                Conservative
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                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200181581-A2.
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                                                                                                                                                                Matches 100;
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patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein of antibodies prolypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAUSS673-AAUS6689 and AAUG7603-AAUG7606.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters from a Bacterium 2412.1 fumonisin catabolic gene cluster. The Bacterium 2412.1 was isolated from maize. The nucleic acid molecules can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters, used for detoxifying fumonisin or related mycotoxin or reducing the pathogenicity of fungi producing fumonisin .
                                                                                                                                                                                                                                                                                                                                                                                                                            6819 goccacggagcectecggeacegegtectegteattggegetggeeeggeetgtet 6878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6879 geogectaccacetegeaatgettggecacgacgtegagatecacgaegggggggggacaaa 6938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gctgtgtacaaattgcgaaagctcagactcaacgccaaaatcttcgagggagccccgat 144
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                          ggcgattgttccgtcgcatgcgacgccatcatcgttggagccggcctcagcggcatctct 84
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                                                                                                                                                                                                                                                                                                               Length 10524;
                                                                                                                                                                                                                                                   Sequence 10524 BP; 2239 A; 3454 C; 2968 G; 1862 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavin monooxygenase fccC nucleotide sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                             Score 41.4; DB 23;
Pred. No. 0.13;
0; Mismatches 61;
                                                                                                                                                                                                               ftp.w1po.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6939 gtcggcggcatgatgcgct 6957
                                                                                                                                                                                                                                                                                                           Query Match 2.5%;
Best Local Similarity 56.1%;
Matches 78; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 tttggcggcgtctggcact 163
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producting an enzyme for detoxifying fumonisin or a structurally related mycotoxin, e.g. in harvested grain, or processed grain which is to be used as animal feed or sliage. Ruminal microorganisms trensformed with the nucleic acid molecules can be used as problotic compositions or as feed inoculant compositions. Plants transformed with the nucleic acid molecules can degrade or transport fumonisin. The plants may be e.g. molecules can degrade or transport fumonisin. The plants may be e.g. maize, sordhum, wheat, tomanch, sovybean, alfalfs sufflower, Brassica, cotton or rice. The products can also be used as detection reagents for tumonisins and related compounds. AAZ91253 represents the Bacterium 2412. I fumonisin catabolic gene cluster, and AAZ91254 to AAZ91273 represent isolated nucleic acids from Bacterium 2412.1 which encode AAY80085 to AAX80104. AAZ91286 from Bacterium 2412.1 which encode AAY80085 to AAX80104. AAZ91286 from AAZ91274 to AAZ91286 are given in the sequence listing from the present specification but are not specifically mentioned further.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 gtatotoattotogotacygggttgctccacagygaagcacactcccgcactcccggcct 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 geatetggteetggegaegggeaaegeeggeaageegeegtteegegetteaagggeea 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 aggacggcgcgtggccgtgatcggatcgaactaggcccacgacatctgcgcagacet 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 gggccagagagtcgccgtcatcggtgccggggccacaagcatccagattgttcaggagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 cgccgatttcaacgggaaggtgattcattcgagtgcctggcacgaagacttcgacgcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterium 2412.1; maize; detoxification; degradation; carcinogen; fumonisin catabolic gene cluster; antifungal; mycotoxin; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 40.2; DB 21; Length 1677; 48.5%; Pred. No. 0.11; tive 0; Mismatches 118; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 ggccaagaaggctgaccaggtaaccatgtttatgcgaaggccgagctat 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570 cgtggcccacggcgttgacgtcaccatgatccagcgcagttcgacccat 618
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1677 BP; 292 A; 541 C; 530 G; 314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterium 2412.1 fumonisin-catabolising gene cluster.
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Matches 111; Conserv
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W0200162286-A1

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The present invention describes isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters from a concode fumonisin catabolic gene cluster. The Bacterium 2412.1 fumonisin catabolic gene cluster. The Bacterium 2412.1 was isolated from maize. The nucleic acid molecules can be used for producing an enzyme for detexifying fumonisin or a structurally related mycotoxin, e.g. in harvested grain, or processed grain which is to be used as animal feed or silage. Ruminal microorganisms transformed with the nucleic acid molecules can be used as probiotic compositions or as feed inoculant compositions. Plants transformed with the nucleic acid molecules can degrated or transport fumonisin and can reduce the maize, sorghum, wheat tomato, soybean, alfalfa, sunflower, Brassica, contron or Tice. The products can also be used as detection reagents for fumonisin and related compounds. AAZ91231 sepresents the Bacterium 2412.1 fumonisin actabolic gene cluster, and AAZ9124 to AAZ91273.

Terpresent isolated nucleic acids from Bacterium 2412.1 which encode AAX80085 to AAX90104, AAZ91286 to AAZ91291 represent sequence used in the examplification of the present invention. AAZ91274 to AAZ91285 are given in the sequence listing from the present specification but are not specifically mentioned further.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19523 agcgcagttcgaaggtccgatcctgcactcgagcgcctatcggagcggggctgatttcaa 19582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19583 aggacggcgcgtggccgtgatcggatcgaacaattcggcccacgacatctgcgcagacct 19642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtatctcattctcgctacggggttgctccacaggaagcacactcccgcactcccggcct 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*t6g" a
/*t6g" a
/*tag b
/note | "light chain variable region coding sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; tumor; epithelial; colorectal; pancreatic; breast; lung; carcinoma; K293; immunostimulant; cytostatic; antisense therapy; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgccgatttcaacgggaaggtgattcattcgagtgcctggcacgaagacttcgacgcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 gggccagagagtcgccgtcatcggtgccgggggccacaagcatccagattgttcaggagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 24494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24494 BP; 4198 A; 7837 C; 8074 G; 4383 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 ggccaagaaggctgaccaggtaaccatgtttatgcgaaggccgagctat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.2; DB 21;
Pred. No. 0.48;
0; Mismatches 118;
                  Claim 29; Page 71-88; 181pp; English.
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les 111; Conservative
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The invention provides a binding structure, such as an antibody, binding to tumor cells, especially epithelial tumor cells such as colorectal, paraetic, breast or lung carcinoma cells. The binding structures, target structures to the binding structures or the substances, i.e. antisense oligonucleotides and ribozymes, are useful in the therapy and in vitro histopsthological diagnosis and prognosis of human malignant disease. The present sequence represents the nucleotide sequence of antibody directed against K293 superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 getecacaggaagcacactecegeacteceggeetegeegatteaaegggaaggtgat 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 gitcicccigaagcigaccictgigaccgccgcgggacacggccgigtaitacigigcgag 680
                                                                                                                                                                                                                                                 A binding structure, such as an antibody, binding to tumor cells, especially epithelial tumor cells such as colorectal, pancreatic, breast or lung carcinoma cells, useful in the therapy, diagnosis and prognosis of human malignant disease
                                                                                                                                                                       Tordsson MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 747 BP; 149 A; 216 C; 211 G; 171 T; 0 other;
                                                                                                                                                                       Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.6; DB 22;
Pred. No. 0.46;
0; Mismatches 54;
                                                                                                                                                                       Nilson BHK,
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 26, 2002, 19:23:31; Search time 7811.87 Seconds (without alignments) 4387.895 Million cell updates/sec	<pre>Title:</pre>	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1797656 seqs, 10463268293 residues	Total number of hits satisfying chosen parameters: 3595312	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:*		4: gb_om:* 5: gb_ov:*	6: gb_pat:* 7: gb_ph:*	8: 9b_pl:* 9: 9b_pr:* 10: qb_pr:*	11: 942-10: **	12: 90_sy:* 13: 90_un:* 14: 90_vi:* 15: em_ba:*							Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the tetal score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description

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tiggocaagaaggtgaccaggtaaccatgttatgcgaaggccgagctattgtctgcc 660 [[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[[	RESULT 2 AXO76842 LOCUS LOCUS DEFINITION ACCESSION VERYWORDS KEYWORDS SOURCE ORGANISM	AX076842 1691 bp DNA linear PAT 22-FEB-2001 Sequence 1 from Patent W00105980. AX076842 AX076842 6I:13121517 Exophiala spinifera
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/note="similar to short-chain alcohol dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 51.4%; Pred. No. 1.5e-68; 5; Conservative 0; Mismatches 716; Indels
                                                                                                                                               502. .2154
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1. 3715
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/gene="cpmB"
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                                             actggaaccgctaccctggcgctcgtgttgattcggagacg---cccttctaccaactga 217
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                                                                                                                                                                                                                                                                                                                                                                                                                 eggetggecatgttgegaeggeaaagtateteattetegetaeggggttgeteeaeagga 457
                                                                        acattcccgaagtatggaaagactggacctggtcttgccgctatcctgaccagaaagagt
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Rhodococcus rhodochrous gene for steroid monooxygenase, complete
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Itaqaki, B., Moril.S. and Iwami, M.

Itaqaki, B., Moril.S. and Iwami, M.

Submitted (16-JAN-1998) Eiji Itaqaki, Kanazawa University, Faculty of Science, Depertment of Chemistry; Kakuma machi, Kanazawa, Rillyawa 920-11, Japan (E-mail:itaqakiecacheibm.s.kanazawa-u.ac.jp, Tel:08-076-264-5685, Fax:08-076-264-5742)

Location/Qualifiers
1885 GATCTGCTGATCCAGCTGATGAACTACCTACGCGACAACAACATCTCGCGCGTCGAAGCC 1944
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                                                                                                                                                                                                                                                                                                                                                                                                                    steroid monooxygenase.
Rhodococcus rhodochrous (strain:IFO3338) DNA.
Rhodococcus rhodochrous
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sawamoto, S., Yamauchi, Y., Miyamoto, M., Iwami, M. and
                                                                                           1945 CAGTCCGAGGCACAGGAAGAAFGGAGCAAGCTGATCGCAGACTTCTGGGACAGCTCGCTG
                                          1423 acgaaatcagcacaagaggcatggtcgattatgattgccaagatgaacgagcacactctg
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Similarity 49.2%; Pred. No. 1.38-49;
Sb. Conservative 0; Mismatches 774; Indels 18;
                                                                                                                                                                1483 ttccccttgacggattcgtggtggactggaggcaacatccctgggaa 1529

    1842
/organism="Rhodococcus rhodochrous"

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Moril,S., S
Itagaki,E.
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AUTHORS
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MEDLINE
REFERENCE
AUTHORS
TITLE
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// profugstrgytypcywgrypcywgryperyvelarogslpklpfinabgvnbgrypcymg
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PGGRIGDEPDVARI TAAPITYDDGCLALDEGNWIANTVONDATRIABGGSILDRYDFAN
PRGIFAVALGGGDGKTLFLCAAPDWDBGARSKAREGRMLATTVAVPHAGRP"
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Ygene="chimb2"
/note="flavin-dependent monooxygenase; contains FAD;
requirss NADPH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4908. ,5543
/gene="chnc2"
/note="putative function as caprolactone hydrolase"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note~"similar to sigma54-dependent transcriptional
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complement(7660, .7998)
/note="similar to ArsR-type regulators"
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/rransl_table=11
/product="cyclohexanone monooxygenase
/protein_id="AAG01290.1"
/db_xref="GI:9864060"
/note="zn-type alcohol dehydrogenase"
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Brevibacterium sp. HCV cyclohexanone oxidation gene cluster 2,
complete sequence.
AP257215
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Brevibacterium sp. HCU.
Brevibacterium sp. HCU
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetalas; Micrococcineae; Brevibacteriaceae; Brevibacterium.
1 (bases 5839 to 7428)
Brzestowicz_P.C., Gibson,K.L., Thomas,S.M., Blasko,M.S. and
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Brzostowicz, P.C., Blasko, M.S. and Rouviere, P.E.
Identification of Two Gene Clusters Involved in Cyclohexanone
Brevibacterium sp. HCU
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                                                                                                                                                                                                                                   /translation-"MRTLDHPSRDEMRLDTVLAALADPVRRTVACKLNDAFGDHACAT
FELPVSKSTATYHFRTLREAGVIRQEYEGTKIMNTCARTIDARFPGSGRVFAAQDIER
                                                                                                                                                                                                                                                                                                                          VGPGYQTTLAAGVRQGSGLPTAAVGLISEPFQGEHILATGQADVILVGREYLRDPNFA LAADALKPFDIDVRFATAXY.
complement(9367,.10154)
/note="similar to gatR-family transcriptional regulators"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLQMLGRDPTVKAPASPPRRRSAGDRHRHGQPRIPCDVADPWR
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VNILGAFLLGLLLDSLARSGPDERWRRRTRILVGTGFWGGPTTYSALAADTAGRLGAG
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                                                                                                                                      proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_except=(pos:complement(10435. .10437),aa:Met)/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  totggcactggaaccgctaccctggcgctcgtgttgattcggagacgcccttctaccaac 214
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                                                                                                                       8198. .9271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 227.6; DB 1; Length 11471;
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3683 c 3786 g 1967 t
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LVEGTIEIRRAESHQTPIVERSMRCNADACRGSQAFGGGSQDHMGENAPSSETAHVRL
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4161. :5306
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ALSIALIDLSGVVRDAMTESPFFTFDRSAALTRLETRAALDRSALGVGVAA
SGFFTGLRQLMTPLSAHGWALSDLDAEFSARLGLFYNDNGGNAAAGBERLGVGVAA
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LSSFAYLLVGRGLGGGVVLDHSLWRGRNGGAFTGLLSPDRRADRFTLGLLREMFAA
LVDALLGGASYSVTERWRKRTAPFELDASIANTDNGBAASNJGGRATPA
LVDALLGGASYSVTRDRFTFILLRSQVVRDVTALGAASNPFSGHFF"
complement(1269..1475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Enclaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and
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Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J.,
Heldelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potcocka, I.,
Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B.,
Laub, M.T., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L.,
Haft, D.H., Kolonoay, J.F., Smit, J., Craven, M., Khout, H., Shetty, J.,
Berry, K., Utterback, T., Tran, K., Wolf, A., Vanathevan, J.,
Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and
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Submitted (31-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1412 ccgttgaggcgacgaaatcagcacaagaggcatggtcgattatgattgccaagatgaacg 1471
                            7265 GGTTCGAATCCACCGAAGAGGTCGAGAATGGCGCCCCATGTCGACACTTTCG 7324
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
Caulobacter.
1 (bases 1 to 11094)
                                                                                        1472 agcacactetgtteecettgaeggattegtggtggaetggaggeaacateetgggaa 1529
                                                                                                                     protein family HMM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of Caulobacter crescentus
Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)
21173698
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/db_xref="taxon:69394"

complement(103..1257)

/gene="CC1792"

complement(103..1257)

/gene="CC1792"

/note="identified by match to prote
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complement(1269. .1475)
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AE005854/c
LOCUS
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SOURCE
ORGANISM
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VERSION
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AUTHORS
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REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
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                            ANLFTVMARTDPNTKGGAGVSAFLVPADLPGLSVGRPEKKNGGGGAHIHDVVFEDVRY
PPUBNIGAGREGGFTVAMRYLDRGRWHLSAVCVGARELLAGVARASERKGFGOPIAS
FOLIGAMIADSKTEALAKKAUYEDTARKRDAGANVTLEAAATKLFASEWGRVADRAV
OVFGGAGTVADYGLERLYRDVRIFRIYEGASGIQOLIIARETLKRGG"
                                                                                                                                                                                                                                                                                                                         'n
a<u>QKARWLPSIASGETITAFALTEAEAGSDSASVQTRAVRDGDHYVLNGVKRYITNAGR</u>
                                                                                                                                                                                                                                                                                                                         Gaps
                                        PFAM protein family
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Pred. No. 4.6e-43;
0; Mismatches 799; Indels 18;
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                                        match to
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complement (5369. 7039)
                                       /note-"identified by PF00743"
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12.8%;
Best Local Similarity 48.1%;
Matches 757; Conservative
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6992 CGACGCCCTTGTGATCGCGCGCGCCTTCGCGCGCATGTACGCCGTTCACACGCGG 6933 cgacgccatcatcgttggagccggcctcagcggcatctctgctgtgtacaaattgcgaaa 104

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 191; DB 1; Length 261
llarity 47.4%; Pred. No. 3.76-36.
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                                                                                                                                                                                                                                                                                                                                                                                                          449
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Actinomycerales; Corynebacterineae; Nocardiaceae; Rhodococcus.
1 (bases 1 to 2618)
Van der Vlugt-Bergmans, C.J.B., Leer, R.J., Gottschalk, G. and van der
Werf, M.J.
The genes involved in immonene and carveol degradation in
Rhodococcus erythropolis DCL14 are localized on a large linear
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Van der Vlugt-Bergmans, C.J.B.
Direct Submission
Submitted (02-JAN-2001) Van der Vlugt-Bergmans C.J.B., Industrial
Microbiology, Wageningen Agricultural University, Bomenweg 2, 6703
HD Wageningen, NETHERANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RER303350 2618 bp DNA linear BCT 06-JUN-20
Rhodococcus erythropolis partial ORF1 for putative
cyclase/dehydrogenase and ORF2 for Baeyer-Villiger monooxygenase
gaaagatggcatatctacttatatgggagtetteteteatggetteeccaatgeettett 1298
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Baeyer-Villiger monooxygenase homologue; cyclase/dehydrogenase;
ORF1; ORF2.
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//gene="chnA"
3439. .24170
//gene="chnA"
//EC_number="1.1.1.1"
//note="dehydrogenase; catalyzes conversion of cyclohexanol
to cyclohexanone in the cyclohexanol oxidation pathway,
approximately 30 nucleotides missing from 3'-end"
//codon_start=1
//transl_table=11
                                                                                                                                                1 (sites)
van Beilen,J.B., Fritsche,U., Seeger,M., Smits,T.H.M. and
Witholt,B.
Cloning of Baeyer-Villiger monooxygenases from Comamonas,
Xanthobacter and Rhodococcus via PCR with highly degenerate primers
                                                                                              subdivision; Rhizobiaceae group;
6-hexanolactone hydrolase; chnA gene; chnB gene; chnC gene; cyclohexanol dehydrogenase; cyclohexanone 1,2-monooxygenase. Asathobacter flavus.
Xanthobacter flavus.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae gI
                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01 NOV-2001) van Beilen J.B., Institute of
Biotechnology, ETH, ETH-Hoenggerberg, CH-8093, SMITZERLAND
Location/Qualifiers
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//do_xref="taxon:281"
complement(<50..>514)
/note="encodes an internal fragment of
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/gene="chnB"
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2 (bases 1 to 4170)
van Beilen,J.B.
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Cloning of Baeyer-Villiger monooxygenases from Comamonas,
Xanthobacter and Rhodococcus via PCR with highly degenerate primers
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van Beilen, J.B.
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AE005856 1 G1:1348 bp DNA linear BCT 28-MAR-2001 caulobacter crescentus section 182 of 359 of the complete genome. AE005866 AE0058573 G1:13423248
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                        1446 ACCGTCACCGGAACGCCTGTCGCGCTGTACAACAACGCGCTCGCCATCGAGGAT 1387
1297 ttcgtcgcccaggctcaagccccgaccgtcctttccaacggcccaacgatcatagaaacc
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                                                                                                                                                                                                                                      atggttgacaaaaaggccaaccgactggtctatgacttctgggccaaaaagactcgatct
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      /codon_start=1
/transl_table=11
/product="putative steroid monooxygenase
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Best Local Similarity 47.3%;
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fgene CC1817.

Anote—"ldentified by Glimmer2; putative"

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Gaulobacter crescentus
Gaulobacter rescentus
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Caulobacter.
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Fraser, C.M.

Direct Submission

Submitted (31-JAN-2001) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Location/Qualifiers

1. 12348

/ Objanism="Caulobacter crescentus"

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152. 1657

/ sene="CC1813"

152. 1657

/ con="CC1813"
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/rote-"identified by match to PFAM protein family HWM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of Caulobacter crescentus
Proc. Nutl. Acad. Scl. U.S.A. 98 (7), 4136-4141 (2001)
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Complete ge
                                               ORGANISM
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AUTHORS
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JOURNAL
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MEDLINE
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AUTHORS
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FEATURES

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CDS

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complement (10632. .11642)
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Llarity 46.5%;
Conservative
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731;
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Matches
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S 391. .2022  
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  cgacgaaatcagcacaagaggcatggtcgattatgattgccaagatgaacgagcacactc 1480
                                     5137 CCACGCCGAAGCCCAGACCCGGTGGAGCCAGACCGTGGGCGAGATCGCCGACCGCACCC 5078
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1 (bases 1 to 2128)
1 (bases 1 to 2128)
1 (bases 1 to 2128)
Actinetobacter. Peoples, O.P. and Walsh, C.T. Actinetobacter syclophaxanone monooxygenase: Gene cloning and sequence determination
7 Bacteriol. 170, 781-789 (1988)
                                                                                                          472 GAGCTCGAACTTAAGGTTCAGGCTTTTGATAAAGCCACGGATGTCGCAGGTACTTGGTAC
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1. .2128
7. Cognism."Acinetobacter sp. .4db.ref."taxon:472"
391. .2022
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                                            592 GATAAAGAATTACTACAATCGCTAGAAATCAAGAAAAAATATGTGCAAGGCCCTGATGTA 651
                                                                                                                                                                                          340 gctgaggtggttgatgcgcggtatgccagagatctgggcacctggactgtcaagacgtcg 399
                                                                                                                                                                                                                                         712 ACCGCGGTTCAATCGGCTCATTACAACGAAGCAGATGCCTTGTGGGAAGTCACCACTGAA
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/translation-"MSOKMDFDAIVIGGGFGGLYAVKKLRDELELKVOAPDKATDVAG
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YNTFNRDNYRLEDVKANPIVETTENGVKLENGDFVELDMLICATGFDAVDGNVVRMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-AUG-1997) Yoshie Hasegawa, Kansai University, Department of Biotechnology, Pacuity of Engineering; Yamate-cho 3-3-35, Sulfat, Osaka 564, Japan (E-mail:yoshie@ipoku.kansai-u.ac.jp, Tel:+81-06-368-0909, Pax:+81-06-388-8609) Sequence updated (09-Jan-1999).

Location/Qualifiers
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Iwaki,H., Hasegawa,Y., Teraoka,M., Tokuyama,T., Bergeron,H. and
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Acinerobacter cyclohexanone monooxygenase: gene cloning and
sequence determination.
J. Bacteriol. 170 (2), 781-789 (1988)
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Acinetobacter sp. (strain:NCIB 9871) DNA.
Acinetobacter sp.
Racherla; Proteobacteria; gamma subdivision; Moraxellaceae;
Acinetobacter.
                 1300 gtcgccacggctcaagccccgaccgtcctttccaacggcccaacgatcatagaaacccaa
                                                                                         1663 GIGCTIGGACCGAAIGGCCCGI----TIACCAACCIGCCGCCAICAAIIGAAICACAG
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6-oxohexanoate dehydrogenase; chnB; cyclohexanone
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538. .2169
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AB02668

Acinetobacter sp. NCIMB9871 cyclohexanol metabolic gene cluster (chuB, chuE, chuR, orf3, chuA, orf5, chuD, chuC), complete cds.

NB02668.1

AB02668.1

AB0268.1

AB02688.1

AB026888.1

AB02688.1

AB026
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Iwaki, H., Hasegawa, Y., Teraoka, M., Tokuyama, T. and Lau, P.C.
Identification and Characterization of Cyclohexanol Metabolic Genes
from Achnetobacter ap. NCIMB 9871
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Hasagawa,Y. and Iwaki,H.
Hasagawa, Kanal Maki,H.
Direct Submission
Submitted (12-APR-1999) Yoshie Hasagawa, Kansai University,
Department of Blotechnology, Faculty of Engineering; Yamate-cho
Department of Blotechnology, Faculty of Engineering; Yamate-cho
Suita, Oaska 564-6680, Japan
(E-mail:Yoshie@ipcku.kansal-u.ac.jp, Tel:81-6-5368-0909)
[Cocation/Qualifiers]
| Islicoluman="achiechobacter sp. NCIMB9871"
| Attain="MCIMB 9871"
| Attain="MCIMB 9871"
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                                                            1984 TTATTCCCTAAAGCGCAATCCTGGATTTTTGGTGCGGAATATCCCGGGCAAGAAAAACG 2043
                                ctgitccccitgacggaticgiggtggaciggaggcaacatccctgggaaagcaacacgi 1539
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Pred. No. 2e-28;
0; Mismatches 803;
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696; Conservative
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GVOUHGGAGYISEYAIERFYRDVRLFRLYEGTTQIQQVIIARNMIREATO**
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metabolism"
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           Acinetobacter sp. SE19.
Acinetobacter sp. SE19
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
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Cheagy Q., Thomas, S.M., Kostichka, K., Valentine, J.R. and Magazajan, V.
Genetic analysis of a gene cluster for cyclohexanol oxi. actnetobacter sp. strain 5519 by in vitro transposition of Bacteriol. 182 (17), 4744-4751 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 17417)
Cheng, Q., Thomas, S.M., Kostichka, K., Valentine, J.R. and
Magarajan, V.
Direct Submission
Submitted (26-JUN-2000) CRAD, DuPont, Experimental Stat:
E328/B48, Wilmington, DE 19880, USA
Location/Qualifiers
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                                                                                                                   Acinetobacter.
           SOURCE
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PUBMED
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AF282240.1 G1:9965281
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GAAAAGGCATGGCAAACAGGTGGCGGTTTCCGTTTCATGTTTGAAACTTTCGGTGAATTT 1398
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                                                                                                                                                                                                                                       gtocaggoacogtoggttggcatcttgaagtcagcocogagcagoggaggcotattto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1630 AATGGCGATTTCGTTGAATTAGACATGCTGATATGTGCCACAGGTTTTGATGCCGTCGAT
                                                                                                           tggaaggcctactaccccacgctgtttgaagcgagtcgaaagtctcggattggattcccg
                                                                                                                                                                         1219 ATCAAAGACAATTATGACAAAATTTGGGATGGTGTATGGAATTCAGCCTTGCCTTTGGC
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NGVLNVINGDSNISSDNIKERIAGATAGGTVIVAGSGUTFGEVAYAIAOLIPEAGLD-
NGVLNVINGDSNISSDNIKEPIOLIPEAGLAGGTVGKKLAGGASTAKRECCMELGGHA
PVIVCDBADDBAAVEFLAGARKHAMQIVEDAYBGTREYVQEGIYKEFSEKVVLEAKQIKV
GCGLDASSNAFELGILFFFTIGLIFFFTIDHYLERANRLPFGLASCHARGGTK
CNDTOENNDEPEGPIIGLIFFTIGLIFFTEAMAQIVEDAYBGGSTATESKNAHQISYGLE
AGANSINHAGLAALAETEFGGIKDSGFGSEGGIEFFDGYLRTRFITGKN"
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fals., 6949
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Brewibacterium sp. HCV cyclohexanol and cyclohexanone oxidation
gene cluster 1, complete sequence.
AP257514
AF257214.2 GI:14719371
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Actinomycetales; Micrococcineae; Brevibacteriaceae; Brevibacterium.
1 (bases 4057 to 5718)
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3 (bases 4057 to 5718)
S Brostowicz, P.C. and Rouviere, P.E.
Direct Submisted (17-APR-7000) CR&D.
Direct Submisted (17-APR-7000) CR&D.
Direct Submisted (17-APR-7000) CR&D.
Humington, DE 19860-0128, USA
STAGESCHOCK, P.C. and Rouviere, P.E.
Direct Submissed (29-DEC-7000) CR&D. DuPont, PO Box 80328 E328/B46, Wilmington, DE 19880-0128, USA
Sequence update by submitter
On Jul 16, 2001 this sequence version replaced g1:9864057.
I. 10549
I. 10549
Creation/Qualifiers
Creation/Qualifiers
Creation/Creation/Creation Bp. HCU*
//giralimington/Humington/Creation Bp. HCU*
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Brzostowicz,P.C., Gibson,K.L., Thomas,S.M., Blasko,M.S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 cgacgccatcatcgttggagccggcctcagcggcatctctgctgtgtacaaattgcgaaa 104
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                                                                                                                                                                                                                                                                                                                                                                            9132. .9902.
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proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4203 CAACCGCTACCCGGGGGTGCGGACCGACAGCGAGTTCCACTACTACTTTCAGCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 c---gaagtatggaaagactggacctggtcttgccgctatcctgaccagaaagagttgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1323 CGCCTATCTCAATTTCATTGCTGATCGACTTGATCTTCGGAAGGACATTCAGCTCAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 geteagacteaacgeeaaatettegagggageeeegattttggeggegtetggeactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 gaaccgctaccctggcgctcgtgttgattcggagacgcccttctaccaactgaacattcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 tggccatgttgcgacggcaaagtatctcattctcgctacgggggttgctccacaggaagca
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9132. .9902
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4057. 5718
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requires NADPH"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5852. .7096
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                                                                                                                            879 ggttgacaaaggccaacgactgtctatgacttctgggccaaaagactcgatctcg
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Search completed: April 26, 2002, 23:02:13 Job time: 13122 sec

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Word size

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Database :

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BH699067

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African clawed frog.

Xenopus laevis

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;

Amphibia: Batrachia; Anura: Mesobatrachia: Pipoldea; Pipidae;

Xenopodinae; Xenopus.

I (bases 1 to 463)

Kitayama,A., Terasaka,C., Mochli,M., Ueno,N., Shin-1,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ448636 1M0246M21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in X. laevis embryo Expressed genes in X. laevis embryo Unpublished (2001).
Contact: Tadau Shin.i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Wishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshiniegenes.nig.ac.jp.
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100.0%; Pred. No.
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98831498

TAIO05619

A0515861

A0515809

A0515808

B055199

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B18605363
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Best Local Similarity
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         RESULT 1
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LOCUS
DEFINITION
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VERSION
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SOURCE
ORGANISM
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ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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AL73065 T. brucel
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                                                                                                                                            April 26, 2002, 23:14:48; Search time 4999.95 Seconds (Without alignments) 4421.647 Million cell updates/sec
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                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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MA78042
AQ708508
AQ708508
AQ708508
AQ708520
BUSS204
BB451655
AW74752
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                                                                                                            nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_gss_inv:*
em_gss_pin:*
em_gss_vrt:*
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Maximum DB seq length: 200000000
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3: em_esthum:*
5: em_esthu:*
6: em_estpl:*
7: em_estpl:*
6: em_estpl:*
9: gb_est:*
10: gb_fest:*
112: gb_fes:*
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Bequence-tagged connectors: A sequence approach to mapping and scanning the human genome acaning the human genome control that have been set of wallace JC, Hood L Control Mashington Center Conference of Washington Center Conference of Washington Center Conference of Set of 
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AQ708508.1 GI:5417934
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota is Eutheria; Primates; Catarrhini; Hominidae; Homo.
Chases i to 45)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. an
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Bukaryota, Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa: Chordata; Craniata; Perchata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidea; Bovidea; Bos.

(Dases 1 to 232)

Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Gasas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennert, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Bertaa, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.

Sequence evaluation of four pooled-tissue normalized bovine CDNA
                                                                                                                                                                                                                                BJ045552 NIBB Mochii normallzed Xenopus neurula library Xenopus laevis cDNA clone XL004115 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                      African clawed frog.

Xenopus laevis
Eukaryota Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Amphibia: Batrachia; Annra: Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae: Xenopus.

I (bases 1 to 642)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-1,T. and Kohara
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                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
Location/Qualifiers
//organ="Xenopus laevis"
//db_xref="taxon:8355"
//clone="XL004115"
//clone="Lib="NIBB Mochii normalized Xenopus neurula library"
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                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-1 Center: Tes Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Fei: 81-559-81-6856
                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 1.4%; Score 23; DB 10; Similarity 100.0%; Pred. No. 0.67; 23; Conservative 0; Mismatches 0
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/dev_stage="stage 15"
152 c 122 g 214 t
                   0; Mismatches
                                                               BJ045552
BJ045552,1 GI:17369603
                   Conservative
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Chlamydomonas retuhardtii.

Chlamydomonas retuhardtii.

Chlamydomonadaceae: Chlamydomonas.

Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae: Chlamydomonas.

I (bases I to 544)

S Asamizu. E., Miura. K., Kucho. K., Inoue, Y., Fukuzawa, H., Ohyama, K., Makmura, Y. and Tabata. S.

Asamizu. E., Miura. K., Chlamydomonas reinhardtii

Concartion of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

NA Res. 7 (5), 305-307 (2000)

NE S053964

Concact: Erika Asamizu

The First Laboratory for plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu. Chiba 292-0812, Japan

Yana 1532-3, Kisarazu. Chiba 292-0812, Japan

Email: saamizu@kazusa.or.jp/en/plant/.

Email: coation/Qualifiers
                                                                                       1. 451,
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone="Piate=945 Col=8 Row=A"
// Clone="Portor: Parcor-11 Human Male BAC Library"
// Sex="male"
// Orde="Veveror: paace316; Site_1: EcoRI; Site_2: EcoRI;
// Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector EcoRI sites.

45 a 65 c 90 g 151 t
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AV644438
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100.0%; Pred. No. 28;
ive 0; Mismatches 0; Indels
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    544
    /organism="Chlamydomonas reinhardtii"

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Plate: 945 row: A column: 8
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 451.
Location/Qualifiers
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Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
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BOOK STATEMENT OF CONTRACTOR AND SEPLENCE CONN CLOSE 176458 5',

ACCESSION NORSES-21. GI:13916624

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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSS: RPCI-11-233G14.TJ
Cohter_GSSS: RPCI-11-233G14.TJ
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
TRA: 301 838 0208
Exax: 301 838 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ485204

321 bp DNA linear GSS 24-APR-1999
RPCI-11-233G14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-233G14
, DNA sequence.
AQ485204
AQ485204.1 GI:4667252
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BB451655.1 GI:9312690
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1. 321

1. 321

1. 321

/ Oraganism="Homo sapiens"

/ db_xref="taxon:9866"

/ clone="RPCI-11-233014"

/ sex="here:" RPCI-11-233014"

/ coll_type="Lymphocytes"

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Eukaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 321)
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URL.http://genome.gsc.riken.go.jp,
Sasaki, M.: Izawa, M.: Watahiki, M.: Ozawa, K.; Tanaka, T.; Yoneda, Y.;
Matsuura, S.; Carninci, P.; Muramatsu, M.; Okazaki, Y. and Hayashizaki
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uj42dO2 y1 Sugano mouse liver mlia Mus musculus cDNA clone HAME.1999 HAMES.1922595 5' similar to qb:M73490 Mus musculus apolipoprotein E MENA, 3' end (MOUSE); mRNA sequence. Al556742 Al556742.1 G1:4440877 BST.
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Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
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     Length 327;
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     DB 9;
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URL:http://genome.gesc.riken.go.jp,
Carninci, P. Mishiyama, Y. Westover. A., Itoh, M., Nagaoka, S., Sasaki
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Thermostabilization and thermocativation of thermolabile enzymes by
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Corganism="Mus musculus"

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                             louse mouse.

Mus muscula.

Mus muscula.

Mus muscula.

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I (bases I to 327)

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Kiyoswa, H., Kolima, Y., Kondo, S., Koya, S., Kuthihara, C., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuno, Y., Makamura, M., Oda, H., Okazaki, Y.,

Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigawa, C., Sato, K., Shibata, Y., Sugawa, M., Tayawa, A., Shiraki, H., Suzuki, H., Tagawa, A., Shiraki, T., Yoonia, Y., Watahiki, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yokota, T., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Kalaka, Y., Contaci, Yoshida, K., Colhida, Hayashizaki, Y., Contaci, Yoshida, K., Calina, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Contact: Smith TPL
Contact: Smith TPL
Contact: Smith TPL
Contact: ARS, USB Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORMARD: GTTTCCCAGTCACCAT
BACKWARD: GTTTCCCAGTCACCAC
Plate: 106 row: E column: 21
Seq primer: ATTAGGTGACACTARG.
Seq primer: ATTAGGTGACACTARAG.
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[1 (Dases I to 428)

[2] I (Dases I to 428)

[3] Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, R. Anders, R., Kelm, P., Vodkin, L., Erpelding, J., Martin, J., Back, C., Mylle, T. Underwood, K., Hiller, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Glbbons, M., Pape, D., Harvey, N., Schurk, R., Riteer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

[N. Waterston, R. and Wilson, R.

[N. Waterston, Project

[N. Washington University School of Medicine

[Washington University School of Washington University School of Washin
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Glycine max
Elkaryocha; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Bertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA, 1braries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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100.0%; Pred. No. 90;
Live 0; Mismatches 0; Indels
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/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_llb="WARC_2BOV"

/tissue_type="pooled"

/lab_host="bH108"
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Matches 19; Conservative
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Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 384)
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 89;
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Seq primer: custom primer used
High quality sequence stop: 1.
Coation/Qualifiers
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Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and nhl8sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypansonae bruce; (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter. J.C. (Making small
insert libraries for whole genome Shotgun sequencing projects.
Genome Sequencing A Practical Approach, eds. M. Vaudin and B.
Bmail: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.asnger.ac.uk/Projects/T_brucel/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: pancreas; vector: pcwv-sport6; site_1: sall; site_2: not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI249258 440 bp mRNA linear EST 03-FEB-1999 qx53c03.xl NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2005060 3' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HDMAN);, mRNA
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Contect: Robert Strausberg, Ph.D. Genil: cgapbs-remail.nin.gov unknown library type. The Email: cf5 Std Error: 0.00 Seq primer: 400P from Gloco High quality sequence stop: 267.
Location/Qualifiers

//Crganism-Homo sapiens*/
//Crganism-Homo sapiens*/
//Clone="InMacE: 2005060"
//Clone="InMacE: 2005060"
//Clone="InMacE: 2005060"
//Lissue=_Inber="Nation"
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/strain="TREU927"
/db_xxef="taxon:5691"
/clone="151903"
125 C 87 g 134 t
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /nab_nose="Univue"

/note="Wector: Publuescript II SK+; Site_1: EcoRI: Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
from 9-11 day old seedlings that were induced for HR
from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
unicoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after inoculation and their mRNA pooled equally
for cDNA construction. The library was prepared using the
Stratagene pBhuescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an XhoI restriction
sitch. EcoRI adaptors were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The CDNA insert is
protected from XhoI digestion via methylation during first
strand synthesis. The CDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Ecoli ElectroMax DHIOB host cells. Plant
care, incoculations, and library construction were
performed by Steve Clough (Lila Vodkin lab, University of
Illinois).
                      Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memcarlal Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 427.

I . 428

/cration/Qualifiers
I . 428

/cration/Contact: Clone is max
/db_xref="taxon:3847"
/clone="SOUBBAN CLONE ID: Gm-cl074-4504"
/tlssue_type="seedlings induced for HR (bypersensitive response)" and and are are are also in a max of max of max of max of max in a max of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TA151G03Q 435 bp DNA linear GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 151g03, reverse sequence, AL473065 AL473065.1 GI:11838338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Trypanosoma brucei.

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 435)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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1.2%; Score 19; DB 10; Length 428;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 0; Indels
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/lab_host="DH10B"
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KEYWORDS
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0; Gaps

Query Match 1.2%; Score 19; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 93; Matches 19; Conservative 0; Mismatches 0; Indels

Search completed: April 27, 2002, 02:58:36 Job time: 13428 sec

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8488, Ap
724, App
367, App
8481, Ap
376, App
8490, Ap
363, App
8477, App
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APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mandhton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/95,244
PRIOR FILING DATE: Rebruary 27, 1995
PRIOR FILING DATE: Rebruary 27, 1995
PRIOR FILING DATE: September 18, 1997
PRIOR FILING DATE: September 27, 1995
PRIOR FILING DATE: September 27, 1996
PRIOR FILING DATE: September 27, 1996
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Sequence 15122, Application US/10105299
GENERAL INFORMATION:
TITLE OF INVEXTION: Human Secreted Proteins
FILE REPERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEO ID NOS: 15197
SOFTWARE: Patentin removed - See File Wrapper or Palm
SEQ ID NO 15122
LENGTH: 21100
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US-10-105-299-14375
US-10-105-299-14380
US-10-103-295-374
US-10-103-299-8488
US-10-112-699-724
US-10-105-299-8481
US-10-105-299-8481
US-10-105-299-8481
US-10-105-299-84890
US-10-105-299-8477
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US-10-105-299-9177
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0.71;
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10-9-54-02-10B-3305
1 Sequence 3305, Application US/09540210B
1 GENERAL INFORMATION:
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     ORGANISM: HOMO :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-540-210B-3305

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US-09-975-254-13242

US-09-975-254-17647

US-09-975-254-17647

US-09-975-254-17647

US-09-975-254-17647

US-09-975-26-17647

US-09-975-26-17647

US-09-975-26-17647

US-10-116-802-207

US-10-116-802-207

US-10-116-802-207

US-10-116-802-207

US-10-116-802-207

US-10-116-699-559

US-10-112-699-559

US-10-105-299-7312

US-10-105-299-7312

US-10-105-299-8633

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US-10-105-299-80321

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US-10-105-299-80321
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Gapop 60.0 , Gapext 60.0
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1638
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Maximum DB seq length: 2000000000
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Match Length DB
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DR FILING DATE: September 29, 1995
OR APPLICATION NUMBER: 08/824,029
OR FILING DATE: Warch 25, 1997
OR FILING DATE: Warch 25, 1996
OR FILING DATE: Warch 25, 1996
OR APPLICATION NUMBER: 06/015,010
OR APPLICATION NUMBER: 06/015,533
OR FILING DATE: April 10, 1996
OR APPLICATION NUMBER: 06/023,338
OR FILING DATE: July 31, 1997
OR APPLICATION NUMBER: 06/023,308
OR FILING DATE: July 31, 1997
OR PELING DATE: July 31, 1996
OR FILING DATE: May 22, 1997
OR FILING DATE: Way 22, 1997
OR FILING DATE: Way 23, 1996
OR FILING DATE: Way 23, 1996
OR FILING DATE: Way 23, 1997
OR FILING DATE: June 24, 1997
OR FILING DATE: June 24, 1997
OR FILING DATE: June 25, 1996
OR FILING DATE: June 25, 1997
OR FILING DATE: June 25, 1996
OR PHLICATION NUMBER: 06/021, 378
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RELING DATE: FEBRUARY 10, 1998

RELING DATE: FEBRUARY 13, 1997

RELING DATE: FEBRUARY 13, 1997

RELING DATE: REACHARY 13, 1997

RELING DATE: MARCH 4, 1998

RELING DATE: MARCH 5, 1997

RELING DATE: MARCH 14, 1997

RELING DATE: MARCH 1998

RELING DATE: MARCH 11, 1997

RELING DATE: MARCH 1998

RELING DATE: MARCH 1998

RELING DATE: MAY 29, 1998
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Sequence 28990, Application US/09975254
; Sequence 28990, Application US/09975254
; General Engenation Sequence 28990, Application US/09975254
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Plants of TITLE OF INVENTION WINBER: US/09/975,254
; CURRENT APPLICATION NUMBER: US/09/263,191
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 28990 ö ö ó Query Match 1.1%; Score 18; DB 5; Length 261; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 18; Conservative 0; Mismatches 0; Indels Query Match
1.1%; Score 18; DB 5; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels Sequence 32635, Application US/09540210B
Sequence 32635, Application US/09540210B
Sequence 32635, Application
Sequence 32635, Application
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
FILE REFERENCE: PD-1037 CIP FEATURE:
NAME/KEY: misc\_feature
OTHER INFORMATION: Incyte ID No: hu00047457
US-09-540-2108-3305 TYPE: DNA
CRGANISM: Glycine max
CRGANISM: Glycine max
CRHER INFORMATION: Clone ID: 700899231H1
US-09-975-254-28990 PRIOR APPLICATION NUMBER: 09/107,592
PRIOR FILING DATE: June 30, 1998
PRIOR FILING DATE: June 30, 1998
PRIOR FILING DATE: JUNE 1, 1997
PRIOR PEDITOR NUMBER: 09/034,079
PRIOR FILING DATE: June 9, 1998
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SEQ ID NO 3305
LENGTH: 216 23 aagagaaggtggccmatt 40 TYPE: DNA ORGANISM: Homo sapiens RESULT 4 US-09-540-210B-32635 RESULT 3 US-09-975-254-28990 ò a qq

us-09-882-694a-2.rnpn

Sequence 8723, Application US/09975254
GENERAL INFORMATION:
Sequence 8723, Application US/09975254
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 2001-10-12
PRIOR PILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 31255
SEQ ID NO 8723 ö ö Gaps Gaps ö ö Query Match 1.1%; Score 18; DB 5; Length 273; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 18; Conservative 0; Mismatches 0; Indels DB 5; Length 253; 9.6; Indels 1.0%; Score 17; DB 100.0%; Pred. No. 9.6 Live 0; Mismatches ; NAME/KEY: misc\_feature ; OTHER INFORMATION: Incyte ID No: hu01324446 US-09-540-210B-32635 TYPE: DNA
CRGANTSM: Glycine max
COTHER HYDORMATION: Clone ID: 700754933H1
US-09-975-254-8723 PRIOR FILING DATE: March 14, 1997
PRIOR FILING DATE: March 30, 1998
PRIOR FILING DATE: March 30, 1998
PRIOR FILING DATE: March 30, 1998
PRIOR FILING DATE: APPT 11, 1997
PRIOR APPLICATION NUMBER: 09/04, 999
PRIOR FILING DATE: May 8, 1998
PRIOR FILING DATE: May 8, 1998
PRIOR FILING DATE: May 29, 1997
PRIOR PILING DATE: May 29, 1997
PRIOR PILING DATE: May 29, 1997
PRIOR PILING DATE: JULY 398
PRIOR PILING DATE: JULY 398
PRIOR PILING DATE: JULY 398
PRIOR FILING DATE: JULY 398
PRIOR PELING DATE: JULP 3, 1997
NUMBER OF SEQ ID NOS: 35654
SOFWMARE: PERL PROGRAM
SEQ ID NO 32635 RESULT 6 US-09-975-254-13242 : Sequence 13242, Application US/09975254 1586 aagagaaggtggccaatt 1603 193 aagagaaggtggccaatt 210 1291 geettettegtegeeae 1307 62 gccttcttcgtcgccac 78 Query Match
Best Local Similarity 100.
Matches 17; Conservative TYPE: DNA ORGANISM: Homo sapiens RESULT 5 US-09-975-254-8723 ò

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RESULT 9
PCT-10502-050-26
Sequence 26, Application PC/TUS0205706
GENERAL INFORMATION:
APPLICANT: Rohm and Haas Company
APPLICANT: Rohm and Haas Company
APPLICANT: Raplitskaya, Marianna Z.
APPLICANT: Raplitskaya, Marianna Z.
TITLE OF INVENTION: Chimeric retinoid X receptors and their use in a novel ecdyson FILE REFERENCE: A01238
FILE REFERENCE: A01238
FILE REPERENCE: A01238
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/294,819
FRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-540-209B-4551/c
| Sequence 4551, Application US/09540209B |
| GENERAL INFORMATION: GARY L. Breton |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES |
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS |
| FILLE REFERENCE: 2709.1001-001 |
| CURRENT APPLICATION NUMBER: US/09/540,209B |
| CURRENT APPLICATION DATE: 2000-04-04 |
| NUMBER OF SEQ ID NOS: 10444 |
| SEQ ID NO 4551 |
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                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 17; DB 1; Length 531; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 17; Conservative 0; Mismatches 0; Indels
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PRIOR FULLIGATION NUMBER: US 60/294,819
PRIOR FULLIGA DATE: 2001-65-31
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
LENGTH: 531
TYPE: DNA
PCT-USO2-05706-38
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PCT-US02-05706-26
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; ORGANISM: B.fragilis
US-09-540-2098-4551
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Best Local Similarity
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LENGTH: 681
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PCT-0602-05706-38
PCT-0602-05706-38
Sequence 38, Application PC/TUS0205706
Sequence 38, Application PC/TUS0205706
GENERAL INFORMATION:
APPLICANT: Poblit, Subba R.
APPLICANT: Palit, Subba R.
APPLICANT: Rapitskaya, Marianna Z.
TITLE OF INVENTION: Chineric retinoid X receptors and their use in a novel ecdysone :
TITLE OF INVENTION: based inducible gene expression system
FILLE REPERENCE: A01238
CUBRENT APPLICATION NUMBER: PCT/CUS02/05706
CUBRENT FILING DATE: 2002-02-20
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thomas J.
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT APPLICATION NUMBER: US/09/275,254
FRICE APPLICATION NUMBER: US/09/253,191
PRIOR FILING DATE: 1999-03-05
NUMBER OF EQ. ID NOS: 31255
SEQ ID NO 1747
                        APPLICANT: Bytum, Joseph R.
APPLICANT: Bytum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT APPLICATION NUMBER: US/09/263,191
PRIOR APPLICATION NUMBER: US/09/263,191
PRIOR FILING DATE: 1999-00.55
NUMBER OF SEQ ID NOS: 31255
SED ID NO 31322
LENGTH: 263
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; ORGANIZNH: Glycine max
:: OTHER INFORMATION: Clone ID: 700907418H1
US-09-975-254-13242
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; ORGANISM: Glycine max
: OTHER INFORMATION: Clone ID: 700954584H1
US-09-975-254-17647
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        GENERAL INFORMATION:
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US-09-975-254-17647
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Core Stuart, Susan G.
APPLICANT: Mullahy, Core J.
APPLICANT: MULLANG DATE: 100,04-03
BRIOR FILING DATE: November 18, 1997
PRIOR APPLICATION NUMBER: 08/395,244
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100.0%; Pred. No. 10;
ive 0; Mismatches 0; Indels C
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100.0%; Pred. No. 10;
Live 0; Mismatches 0; Indels
                          Sequence 13829, Application US/10105299
; Sequence 13829, Application US/10105299
; GENERAL INFORMATION:
    TITLE OF INVENTION: Human Secreted Proteins
; FILLE REFERENCE: PS$50
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILLIG DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13829
; LENGTH: 9702
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US-105-299-13828
Sequence 13828, Application US/10105299
Sequence 13828, Application US/10105299
GENERAL INFORMATION:
TITLE OF INVENTION: Human Secreted Proteins
FILE REFRENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT PILING DATE: 2002-03-26
NUMBER OF ESO ID DATE: 2002-03-26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13828
LENGTH: 27976
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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CORGANISM: Homo sapiens
US-10-105-299-13828
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CORGANISM: Homo sapiens
US-10-105-299-13829
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US-09-540-210B-21427
RESULT 13
US-10-105-299-13829
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Pred. No. 10;
Mismatches 0; Indels
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Pred. No. 10;
0; Mismatches 0; Indels
                                                                               RESULT 11
US-10-116-020-157
Sequence 157, Application US/10116802
Sequence 157, Application US/10116802
GENERAL INFORMATION:
APPLICANT: Amy Lasek
TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REPERENCE: PA-0045 US
CURRENT APPLICATION UNMER: US/10/116,802
CURRENT APPLICATION UNMER: 00/281,593
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
SOFTWARE: PERL PROGRAM
SEQ ID NO 157
LEMENTH: 4874
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVESTIGATION GENES EXPRESSED IN LUNG CANCER;
TITLE OF INVESTIGATION WUBBER: US/10/116,802
CURRENT APPLICATION NUMBER: US/10/116,802
CURRENT APPLICATION NUMBER: 60,281,593
PRIOR FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
SOOTWARE: PERL PROGRAM
SOOTWARE: PERL PROGRAM
SOOTWARE: TENGTH: 7182
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; OTHER INFORMATION: Incyte ID No: 1099945.13
US-10-116-802-207
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
NAME/KEY: unsure
LOCATION: 4822
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100.0%; Pred. No.
tive 0; Mismatc
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Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                5287 atcatcgttggagccgg 5303
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ORGANISM: Homo sapiens
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Matches 17; Conserv
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US-10-116-802-207
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us-09-882-694a-2.rnpn

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PRIOR FILING DATE: February 27, 1995
PRIOR FILING DATE: September 27, 1996
PRIOR FILING DATE: September 27, 1996
PRIOR FILING DATE: September 29, 1995
PRIOR FILING DATE: SEPTEMBER: 60/065,526
PRIOR PLING DATE: SEPTEMBER: 60/014, 029
PRIOR PLING DATE: MEACH 25, 1996
PRIOR PAPLICATION NUMBER: 60/015,533
PRIOR PAPLICATION NUMBER: 60/015,533
PRIOR PAPLICATION NUMBER: 60/015,533
PRIOR PAPLICATION NUMBER: 60/012,109
PRIOR PAPLICATION NUMBER: 60/013,109
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Gaps ö Query Match 1.0%; Score 16; DB 5; Length 204; Best Local Similarity 100.0%; Pred. No. 36; Matches 16; Conservative 0; Mismatches 0; Indels ; NAME/KEY: misc\_feature or OTHER INFORMATION: Incyte ID No: hu00323909 15-09-540-210B-2147 PRIOR APPLICATION NUMBER: 09/074,999
PRIOR FILING DATE: May 8, 1998
PRIOR FILING DATE: May 8, 1998
PRIOR FILING DATE: May 29, 1997
PRIOR FILING DATE: May 29, 1997
PRIOR FILING DATE: June 30, 1998
PRIOR FILING DATE: June 30, 1998
PRIOR PILING DATE: June 30, 1997
PRIOR PILING DATE: June 9, 1997
PRIOR APPLICATION NUMBER: 60/049,079
PRIOR PILING DATE: June 9, 1998
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SCOFTWARE: PERL PROGRAM
SEQ ID NO 2147 Search completed: April 27, 2002, 07:43:52 Job time: 17084 sec TYPE: DNA ORGANISM: Homo sapiens ò

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
/cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
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US-09-351-224E-2
Sequence 2, Application US/09351224E
GENERAL INFORMATION:
APPLICANT: Maddox, Jon
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Compositions and Methods if TITLE OF INVENTION: Detoxification
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224E
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1638
                                                                                                                                                                                                      100.0%; Score 1638;
.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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NAME,KEY: misc_feature

LOCATION: (0) ... (0)

OTHER INFORMATION: flavin monooxygenase,
US-09-351-224E-2
                                                                                                                                                       TYPE: DNA
ORGANISM: Exophiala spinifera
                          cttcatgctccctgctaa 1638
                                 Query Match
Best Local Similarity
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                                                                                     APPLICANT: Duvick, Jon
TTLE OF INVEKTION: Compositions and Methods for Furmonisin Detoxification
FILE REFERENCE: 5118-56
CURRENT APPLICATION NUMBER: US/09/351,823
CURRENT PILING DATE: 199-07-12
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
LENGTH: 1638
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches
                                                                       Sequence 2, Application US/09351823 GENERAL INFORMATION:
                    TYPE: DNA
ORGANISM: Exophiala spinifera
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US-09-351-823-2
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APPLICANT: Duvick, Jon APPLICANT: Maddox, Joyce APPLICANT: Gilliam, Jacob APPLICANT: Folkerts, Otto
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US-09-677-488-2
| Sequence 2. Application US/09677488|
| SEMERAL INFORMATION:
| APPLICANT: Duvick, Jon |
| TILLE OF INVENTION: Compositions and Methods for Fummonisin Detoxification |
| FILE REFERENCE: 3579/20410 (5718-111A )
| CURRENT PELLIANTON NUMBER: US/09/677,488 |
| PRIOR PILIAG DATE: 2000-10-02 |
| PRIOR PILIAG DATE: 1999-07-12 |
| NORMER OF SEQ ID NOS: 11 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 2 |
| LENGTH: 1638 |
| LENGTH: 1638 |
| SED ID NOS: 10-02 |
| SED ID NOS: 10-02 |
| LENGTH: 1638 |
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US-09-677-488-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches
                                                                                                                                                            TYPE: DNA
ORGANISM: Exophiala spinifera
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US-09-677-682-2
; Sequence 2, Application US/09677682
; GENERAL INFORMATION:
APPLICANT: DUVICK, Jon
TITLE OF INFURINCY. Compositions and Methods for Fummonisin Detoxification
FILE REFERENCE: 35738/204101 (5718-1118)
CURRENT APPLICATION NUMBER: US/09/677,682
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          for Fumonisin
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                                                                                                           NAME/KEY: misc_feature
LOCATION: (0)...(0)
| THER INFORMATION: flavin monooxygenase, fully spliced
US-09-677-4888-2
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APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Defoxification
FILE REFERENCE: 35718/204100
CURRENT APPLICATION NUMBER: US/09/677,488A
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR PILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTMARE: FastSEQ for Windows Version 4.0
           Methods
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11arity 100.0%;
Conservative 0;
                                                                                        TYPE: DNA
ORGANISM: Exophiala spinifera
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Matches 1638; Conserv
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LENGTH: 16
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                                   CRGANISM: Exophiala spinifera
FEATURE:
CTHER INFORMATION: flavin monooxygenase, fully
US-09-677-682-2
                                                              DB
                                                             Score 1638; 1
Pred. No. 0;
; Mismatches
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1638
                                                             Query Match
Best Local Similarity 100.0%; Partches 1638; Conservative 0;
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195-09-67-682A-2
Sequence 2, Application US/09677682A
Sequence 2, Application US/09677682A
SEQUENCE 1NFORMATION:
APPLICANT: Maddox, Joon
APPLICANT: Gilliam, Jacob
APPLICANT: Creats, Otto
TITLE OF INVENTION: Compositions and Methods 1
TITLE OF INVENTION: Detcxification
FILE REPERENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,682A
CURRENT FILING DATE: 2000-10-02
FRIOR APPLICATION NUMBER: 09/351,224
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APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Grasta, Otto
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Detoxification
TITLE OF INVENTION: Detoxification
CURRENT APPLICATION NUMBER: US/09/677, 682B
CURRENT APPLICATION NUMBER: 09/351,224
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                                           NAME/KEY: misc_feature

LOCATION: (0) ... (0)

CTHER INFORMATION: flavin moncoxygenase, US-09-677-682A-2
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PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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llarity 100.0%; Pi
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                              TYPE: DNA
ORGANISM: Exophiala spinifera
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APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions
FILE REFERENCE: 35718/208255
CURRENT APPLICATION NUMBER: US/09/882,694
CURRENT FILING NAMER: US/09/882,694
PRIOR APPLICATION NUMBER: US/09/882,694
                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09882694 GENERAL INFORMATION:
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                                              NAME/KEY: misc_feature

LOCATION: (0)...(0)

CTHER INNOMATION: flavin monooxygenase, fully

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                                                                                 100.0%; Score 1638;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 2
                              TYPE: DNA
ORGANISM: Exophiala spinifera
                                                                                 Query Match
Best Local Similarity
Matches 1638; Conserv
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GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods of INVENTION: Detaxification
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/882,694A
CURRENT APLICATION NUMBER: 2001-06-15
PRIOR APPLICATION NUMBER: 99/351,224
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                               TYPE: DNA
ORGANISM: Exophiala spinifera
FATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
CHER INFORMATION: flavin monooxygenase, fully spliced
US-09-882-694-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1638; Conservative 0; Mismatches
             4.0
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ 1D NOS: 11
SOFWARE: PastSEQ for Windows Version
SEQ 10 NO 2
LENGTH: 1638
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT DAVIGE. JOHN STATE OF THE REPERBERGE: 5718-111
CURRENT APPLICATION WHERE: US/09/351,224
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1.2
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                                                            100.0%; Score 163%;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                  NAME/KEY: misc_feature
| LOCATION: (0)...(0)
| CTHER INFORMATION: flavin monooxygenase,
05-09-882-6948-2
         4.0
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOCTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 1638
                      TYPE: DNA
ORGANISM: Exophiala spinifera
DATE: 1999-07-12
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; OTHER INFORMATION: flavin monooxygenase with intron
US-09-351-224E-1
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APPLICANT: BUVICK, JON
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts Otto
APPLICANT: Craste, Oswald R.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Detxification
FILE REFERENCE: 5718-11
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Exophiala spinifera
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       ; OTHER INFORMATION: flavin monooxygenase with intron US-09-351-224-1
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                                                 72.3%; Score 1184; Dilarity 100.0%; Pred, No. 0; Conservative 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: DUVICK, Jon
TITLE OF INVENTION: Compositions and Methods for Fummonisin Detoxification
FILE REFERENCE: 5718 UMBER: US/09/351,823
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
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ORGANISM: Exophiala spinifera
FEATURE:
OTHER INFORMATION: flavin monooxygenase with intron
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GENERAL INFORMATION:
APPLICANT: DUVICK, Jon
APPLICANT: Maddox, JOyce
APPLICANT: Cilliam, Jacob
APPLICANT: Clasta, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFRENCE: 357187204100
FILE REFRENCE: 357187204100
CURRENT APPLICATION NUMBER: US/09/677,488A
PRIOR FILING DATE: 1999-07712
NUMBER OF FEEL 1999-07712
NUMBER OF FEEL 1999-07712
SEQ ID NOS: 11
SECTION OF SECTION NOS: 11
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GENERAL INFORMATION:
APPLICANT: DUVICK, JON
TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification
FILE REFERENCE: 37718/20100 (5718-111A)
CURRENT APPLICATION NUMBER: 09/09/677,488
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR PILING DATE: 1099-07-12
NUMBER OF SEQ ID NOS: 11
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                                                                   ) OTHER INFORMATION: flavin monooxygenase with intron US-09-677-488-1
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ORGANISM: Exophiala spinifera
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; LOCATION: (0)...(0); | LOCATION: f. POTHER INFORMATION: f. TOTH 488A-1.
                       DB 26;
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                       Query Match 72.3%; Score 1184; Dest Local Similarity 100.0%; Pred. No. 0; Matches 1184; Conservative 0; Mismatches
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APPLICANT: Filtemann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Kumagai, Monto H.
TITLE OF INVENTION: DAS BOUGENCES ENCODING ENZYMES USEFUL IN TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
CORRESPONDENCE: 19
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COUNTRY: ALSA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
FLING DATE:
FLING DATE:
FLING DATE:
FLING DATE:
FLING TOWNER: US/08/579,667
FLING DATE:
FLING TOWNER: US/08/579,667
FREERRATION NUMBER: 37,092
FREERRATION UNBER: 37,092
FREERRATION FOR TOWNER: 37,092
FREERRATIONE: 919-420-2200
FREERRATIONE: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
US-08-370-223-6

US-08-998-416-54

US-08-998-416-135

US-09-007-119-17

US-09-007-119-16

US-08-096-18-24-16

US-08-877-109-1

US-08-877-109-1

US-08-877-109-1

US-08-877-109-1

US-08-870-170A-6

US-09-565-69-6

US-09-565-69-6

US-09-565-69-6

US-09-818-112-11

US-08-818-112-11

US-08-818-112-11

US-08-818-112-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                 US-08-726-462B-1
US-08-642-330-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charlotte
No. 5705624th Carolina
X: USA
                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-08-579-667-7/c
Sequence 7, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1814 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   CDS
363..1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
   NAME/KEY:
; LOCATION:
US-08-579-667-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
    Query Match
   22666666666644444
200012646666644444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 117, App
Sequence 286, Appli
Sequence 124, Appli
                                                                                                April 27, 2002, 01:38:33 ; Search time 151.01 Seconds (without alignments) 2664.378 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                          US-09-882-694A-2
1638
1 atgtcggccaccagcaactc......tgcttcatgctccctgctaa 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                    OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *
Ouery
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                           Word size :
                                                                           OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                          Sequence:
                                                                                                      Run on:
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1.0%; Score 17; DB 1; Length 845; 100.0%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-748-725-1/C
Sequence 1, Application US/08748725
Sequence 1, Application US/08748725
Sequence 1, Application US/08748725
Setent No. S859346
APPLICANT: Zhang et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: ...ton
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READALE FORM:
MEDLUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER READALE FORM:
MEDLUM TYPE: 3.5 Diskette, 1.44 Mb
COMPATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,451B
FILING DATE: 23-JUNE-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: LECHY, Karen F.
RECEISTRATION NUMBER: 00786/219001
TELECOMMUNICATION INFORMATION:
TELECHAMATION FOR SEQ ID NO: 1:
TELECOMMUNICATION INFORMATION:
TELECHAMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 845
TINFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 845
TURDEN TO THE SEC ID NO: 1:
STRANDEDNESS: $1091e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
2.1P: 0.2110-2804
COMPUTER READALE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNMBER:
ATTORNEY CAGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/POCKET UNMBER: 00786/219002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 44
Mismatches
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Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-266-451B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                           RESULT 2
US-08-562-985A-8/C
US-08-562-985A-8/C
Sequence 8, Application US/08562985A
Ferent No. 5821657
GENERAL INFORMATION:
APPLICANT: CHIANG, John Y.L.
TITLE OF INVENTION: CHOLESTEROL 7ALPHA-HYDROXYLASE EXPRESSION AND A TITLE OF INVENTION: CHOLESTEROL 7ALPHA-HYDROXYLASE EXPRESSION AND STITLE OF INVENTION: CHOLESTEROL 7ALPHA-HYDROXYLASE EXPRESSION AND A TITLE OF INVENTION OF ITS REGULATORY ELEMENTS
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLLY & Lardher
STREET: 3000 K Street, N.W., Sulte 500
CITY: Washington
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                              Gaps
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-08-266-451B-1/C
Sequence 1, Application US/08266451B
Fatent WO. 5623054
GENERAL INFORMATION:
APPLICANT: Zhang et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
WUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRL..
STRL..
STATE: D.C.
COUNTY: USA
COUNTY: USA
COUNTUER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: POPPY disk
CONFUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/562,985A
FILING DATE: 27-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
TELEPHONE: (202)672-5399
TELEPHONE: SEQ ID NO: 8:
                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 43;
Mismatches
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
                                                                  TELEFAX: (202)672-5399
TELEX: 90416
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1571 atgagcagatctgtcaa 1587
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US-08-562-985A-8
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Gaps ö

Indels

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0; Gaps

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RESULT 6
US-08-462-109A-5
US-08-462-109A-5
Sequence 5, Application US/08462109A
Patent No. 5802875
Fatent No. 5802875
Fatent No. 5802875
FAPLICANT: Cole, Susan P.C.
APPLICANT: Cole, Susan P.C.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: METHERD RESISTANT TUMOR CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6 COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston Application of Street, Suite 510
CITY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASCII text
COMPUTER: ASCII text
COMPATE: ASCII text
COMPATE: ASCII text
CONFRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/462,109A
FILING DATE: 27-CT-1993
APPLICATION NUMBER: 08/41,893
FILING DATE: 26-CT-1993
APPLICATION NUMBER: 08/41,893
APPLIC
                                                                                                                                                                                                                                                   1.0%; Score 17; DB 1; Length 5889; 100.0%; Pred. No. 44; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Db 3554 GAAGGCCTACTACCCA 3570
                                                                                                                                                                                                                                                                                                                                                                            702 gaaggcctactacccca 718
                                                                                                                                                                                                                                                             0.09 Query Match
Best Local Similarity 100.0
Matches 17; Conservative
STRANDEDNESS: double
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                                                                                                              ; NAME/KEY: CDS
; LOCATION: 6 4589
US-08-463-092B-5
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; LOCATION: 6 4
US-08-462-109A-5
                                  TOPOLOGY: II
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Sequence 5, Application US/08463092B
Patent No. 576680
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Cole, Susan P.C.
TILLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING TITLE OF INVENTION: ISOLATED RESISTANCE PROFEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
STREE: Ontailo
COUNTY: Kingston
STATE: Ontailo
COUNTY: CANADA
ITE: K7L 3N6
COMPUTER: FLORPY disk
COMPUTER: ISOLATED
COMPUTER: ISOLATED
COMPUTER: ISOLATED
COMPUTER: ISOLATED
COMPUTER: ACT T + ACT - DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                   1.0%; Score 17; DB 2; Length 845; 100.0%; Pred. No. 44; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: R.C.LOUDING SOUTHERS SOUTHER STATES OF CORRENT APPLICATION DATA:
APPLICATION UNMER: US/08/463,092B FILING DATE: 05-UN-1995
CLASSIFICATION UNMER: US/08/463,092B FILING DATE: 27-US-1992
CLASSIFICATION DATA: APPLICATION UNMER: 08/029,340
FILING DATE: 3-NAR-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/029,340
FILING DATE: 4-NAR-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/4141,893
FILING DATE: 26-UST-1993
CLASSIFICATION UNMER: 39,399
FILING DATE: 20-MAR-1995
CLASSIFICATION NUMBER: 39,399
REFERRACE/DOCKET NUMBER: 39,399
REFERRACE/DOCKET NUMBER: 01546
TELECPHONIC (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
FROUTH FARM PASSIFICATION INDERMATION: TELECPHONE: (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
FROUTH FARM PASSE DAILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 5889 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 GAAAGCTCAGACTCAAC 317
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        101 gaaagctcagactcaac 117
                                                                                     TYPE: nucleic acid
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLGGY: linear
US-08-748-725-1
                                                                                                                                                                                                                                                                                                                   0.00 Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-463-092B-5
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Gaps
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44;
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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0
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       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-461-384B-5
; Sequence 5, Application US/08461384B
       ö
                                                                          Db 3554 GAAGGCCTACTACCCCA 3570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702 gaaggeetactaceca 718
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11near
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 6 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
US-08-463-179A-5
       17;
       Matches
                                                     ö
                                                     Gaps
                                                     ö
     Length 5889;
                                                                                                                                                                                                                                                                                                               GENERAL INCOMATION:

APPLICANT: Deeley, Roger G.
APPLICANT: Cole Susan P.C.
TITLE OF INVENTION: NETHODS FOR CONFERRING MULTIDRUG
TITLE OF INVENTION: NESISTANCE ON A CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
ADDRESSEE: PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STREET: And ADDRESS: ADDRESS: ADDRESSEE PARTEO RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Gueen's University at Kingston
CITY: Kingston
CITY: Kingston
STREET: Ontario
COUNTY: Kingston
APPLICATION
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS MAD COMPALIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/460,907B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5889;
                                                   0; Indels
Query Match 1.0%; Score 17; DB 2; Best Local Similarity 100.0%; Pred. No. 44; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 17; DB 2; 100.0%; Pred, No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
CLASSIPICATION DATA:
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/02,340
FILING DATE: 8-MAR-1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-0CT-1993
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/41,893
FILING DATE: 20-MAR-1995
CLASSIPICATION: 424
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIPICATION: 424
ATTOREY/AGENT INFORMATION:
REGISTRATION NUMBER: 39,539
REFERENCE/COCKET NUMBER: 01551
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATI
                                                                                                                                                                                                         RESULT 7
US-08-460-907B-5
Sequence 5, Application US/08460907B
Patent No. 5891724
; GENERAL INFORMATION:
                                                                                                                3554 GAAGGCCTACTACCCCA 3570
                                                                                           702 gaaggectactececa 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 6 4589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
US-08-460-907B-5
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Gaps

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Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: State, Haim
APPLICANT: STATE, Haim
APPLICANT: STATE, Haim
APPLICANT: SALORI, MOSHE
TITLE OF INVENTION: TRANSCENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANII-CHOLINESTERASE SUBSTRACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: AD
                                                                       1.0%; Score 17; DB 6; Length 8224;
100.0%; Pred. No. 45;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/814,095
ICLASSITECATION NUMBER: US/08/814,095
CLASSITECATION NUMBER: US/08/814,095
CLASSITECATION NUMBER: 38,972
NAME: MONTGOMETY, 11ene N
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECPHONE: (248) 539-5050
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDENDESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
BESCRIPTION: Acesc = "Cosmid including ACHE
DESCRIPTION: Acesc = "Cosmid including ACHE
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
LOCATION: 22465.,22537
OTHER INFORMATION: /function~ "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:
                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon
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US-08-814-095-7
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FRESULT 10
518080-1
; Patent No. 5180808
APPLICANT: RUGSLAHTI, ERKKI I.
TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
ANTIBODIES, AND METHODS OF DETECTING THE SAME
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/441,179
FILING DATE: 27-NOV-1989
SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Watch
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3554 GAAGGCCTACTACCCCA 3570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
TOCATION: 6 4589
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5180808-1
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US-08-461-384B-5
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RESULT 12
US-09-245-041-5/c
US-09-245-041-5/c
Sequence 5, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: NOOFC, K.; APPLICANT: NOOFC, K.; APPLICANT: NOOFC, K.; APPLICANT: NOOFC, K.; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
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NAME/KEY:
COCATION: complement (31363..31534)
OFHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 14
FEATURE:
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COMPER INFORMATION: /gene="ARS"
US-08-814-095-7
*PEATURE:
NAME/KEY: exon
LOCATION: complement (32569..32628)
OCHER INPORMATION: /genc="AR"
OTHER INFORMATION: /number=7
                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
EACHION: complement (31894..32080)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 9
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NAME/KEY: exon
LOCATION: complement (31131..31284)
OFHER INFORMATION: /gene="AR"
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NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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OTHER INFORMATION: /gene="AR"
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FEATURE:
                                                                                                                                 NAME/KEY: exon
LOCATION: complement (32386..32468)
OCHER INFORMATION: /gene="AR"
OTHER INFORMATION: /rumber="8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: complement (30816..31011)
COTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PERENTE Release #1.0, Version #1.25
SOFTWARRE: PERENTE RESPECTION DATA:
APPLICATION UNBER: 04.35
FILING DATE: 21-SEPT-1994
FILING DATE: 21-SEPT-1994
FILING DATE: 27-NAR-1992
ATPORNEY/ACTION NUMBER: 07/859,072
FILING DATE: 27-NAR-1992
ATPORNEY/ACTION NUMBER: 30/859,072
FILING DATE: 27-NAR-1992
ATPORNEY/ACTION NUMBER: 30/859,072
FILING DATE: 27-NAR-1992
ATPORNEY/ACTION NUMBER: 30/859,072
FILING DATE: 21-SEPT-1994
APPLICATION NUMBER: 30/859,072
FILING DATE: 21-SEPT-1994
APPLICATION NUMBER: 30/859,072
FILING DATE: 30/859,072
FILING DAT
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US-09-103-840A-1/C
IS-09-103-840A-1/C
Sequence 1, Application US/09103840A
Patent No. 624438
GENERAL INFORMATION:
APPLICANT: FILEISCHMAN, Robert D.
APPLICANT: FILEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: USBECOLOSIS
FILE REFERENCE: 4366-2007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENTH: 4411529
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1.0%; Score 17; DB 4; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.0%; Score 17; DB 4; Length 90050; Best Local Similarity 100.0%; Pred No. 45; Matches 17; Conservative O; Mismetches 0; Indels
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US-08-465-798-2

Sequence 2, Application US/08465798

PARENT NO. 568387

GENERAL INFORMATION:
APPLICANT: LU-CHANG, A-Lein
APPLICANT: LU-CHANG, A-Lein
TITLE OF INVENTION: WITH MISMATCH REPAIR ENZYMES
TITLE OF INVENTION: DEPECTION OF GENE MUTATIONS
TITLE OF INVENTION: WITH MISMATCH REPAIR ENZYMES
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
                     CURRENT FILING DATE: 1999-02-05
FRALLER PEPLICATION NUMBER: 60/093,630
FRALLER FILING DATE: 1998-07-21
FEARLIER FILING DATE: 1998-07-21
FEARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASISEQ FOR Windows Version 3.0
LENGTH: 90050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 cettetaccaactgaac 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 CCTTCTACCAACTGAAC 332
                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-245-041-5
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FILLING DATE: 27-WAR-1992
ATTORNEY AGENT INFORMATION:
NAME: KTT, Gordon
REGISTRATION NUMBER: 30.764
REPERROKE/COCKET NUMBER: A-6013-2
REPERROKE/COCKET NUMBER: A-6013-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 29-7060
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 115 base pairs
TYPE: nucleic acid
STRANDEDNESS: $1ngle
TOPOLOGY: linear
MOLECULE TYPE: Synthetic DNA
HYPOTHERICAL: NO
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Search completed: April 27, 2002, 05:54:18 Job time: 15345 sec

Human Human

Drosophila melanog Human ORFX ORF2197 Human CDNA sequenc Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Prococcus abyssi

planctomyces maris
Human secreted pro
Arabidopsis thalia
Mycoplasma hyopneu
Human breast cell
Human breast cell
Human brain expres
Human foetal liver
Probe #1147 used t
Human brone marrow
Probe #1178 for ge
Human brone marrow
Human brone marrow
Rrobe #1178 used t
Human brone marrow

Word size

Searched:

Sequence:

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Human cDNA 5'-end Human cDNA clone r DNA encoding recom DNA encoding novel

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Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permesase; p-dyrooprofein; fimnolisin esterase; detoxification; mycotoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
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/product= "E. spinifera flavin monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exophiala spinifera flavin monooxygenase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                       ABL24809
AAC37255
AAA56852
ABA42792
                                                                                                                                                                                                                                                                           ABA22995
AAK01468
AAK11538
AAI11538
AAI11456
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ABA22671
AAI32492
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AAI32492
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ABL20976
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ABL13554
ABL13534
ABL13932
AAH1224
AAS38063
AAS38063
AAC12316
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1..1638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD02691 standard; DNA; 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US15824.
   99WO-US15824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
1494
1549
2005
20171
20171
20171
4114
4160
48857
34980
                                                                                                                                                                Exophiala spinifera.
   WO200105980-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001.
   AAD02691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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   RESULT
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N.ceneseq_0.1280.2;*

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24. $IDSI_gcgdata_hold_geneseq_geneseq_nembl_NAl1990.DAT;*

24. $IDSI_gcgdata_hold_geneseq_geneseq_nembl_NAl1990.DAT;*
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                                                                                             April 27, 2002, 01:38:37 ; Search time 705 Seconds (without alignments) 3985.086 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                              1 atgteggecaccagcaacte.........tgetteatgeteetgetaa 1638
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                                                                                                                                                                                                                                                                                                       3472872
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                1736436 segs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                    using sw model
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AAD02690
AAV03881
ABA15497
AAF86431
AAZ63301
AAZ63301
ABL20977
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Gapop 60.0 , Gapext 60.0
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1638
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Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal consumption Claim 1b; Page 64; 90pp; English. Maddox J, WPI; 2001-147345/15. P-PSDB; AAY72634. JP, Duvick 

Sequence 1638 BP; 388 A; 432 C; 462 G; 356 T; 0 other;

Exophiala spinifera.

ggagccggcctcagcggcatctctgctgtgtacaaattgcgaaagctcagactcaacgcc 120 gacaagatccggggcttgagaaaagacgtctacttcggagctgaggtggttgatgcgcgg 360 tatgccagagatotgggcacctggactgtcaagacgtcggctggccatgttgcgacggca 420 ggageeggeeteageggeatetetgetgtacaaattgegaaageteagaeteaacgee 120 gacaagatccggggcttgagaaaagacgtctacttcggagctgaggtggttgatgcgcgg 360 Gaps gotogigitigaiticggagacgocottotaccaactgaacattcccgaagtaiggaaagac ö DB 22; Length 1638; 0; Indels Ouery Match 100.0%; Score 1638; Best Local Similarity 100.0%; Pred. No. 0; Matches 1638; Conservative 0; Mismatches Query Match 61 61 121 121 181 181 241 241 301 301 361 361 421 121 a a qq OP g g ò a õ ò δ õ ò ò ò

atctttgaagtcagccccgagcagcggggaggcctatttcgaagagttgtggggagcgtggg attgcaaagttggaggccgagccgccgcgtccgttgaggcgacgaatcagcacaaagg attgcaaagttggaggccgagcacgccacgtccgttgaggcgacgaaatcagcacaagag atgcggcaacgaacgatggataggaacgaacagacagcctggaaggcctactaccccacg atgcggcaacgatggataggaacgaacagacatgcctggaaggcctactcccacg atetttgaagteageecegageagegggaggeetatttegaagagttgtgggagegtggg ctggtctatgacttctgggccaaaaagactcgatctcgtatcgtcaatccggcaaagaga accgtcctttccaacggcccaacgatcatagaaacccaagtcgacttgatcgccgataca 1021 1081 1141 1321 481 541 601 781 901 1021 1081 1141 1201 1201 1261 1261 1321 1441 1441 481 541 601 661 661 721 721 781 841 841 901 196 961 1381 1381 1501 1501 g 6 9 6 ő a õ g ò q 6 6 δ α α g g oy oy ò ద Ś a š QQ οy qq ç q functional degradative or transport enzymes such as flavin monocxygenase, functional sin degradative or transport enzymes such as flavin monocxygenase, aldehyde dehydrogenase, permease and p-glycoprotein. A funchish esterase enzyme with at least one funchish degradative enzyme is useful for enzyme with at least one funchish degradative enzyme is useful for detoxifying fumonish or a structurally related mycotoxin present in harvested grain, on application to a plant or to harvested grain or a structurally related mycotoxin present in during processing, or to processed grain that is to be used as animal of or human feed, or as a slades. Nucleotide fragments of the present invention are useful as probes and primers. They can be introduced into microorganisms that multiply on plants to deliver enzymes to potential target crops: the genes encoding the degrading enzymes are introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the twention are fermented in a bacterial host and the resulting bacteria in spread and used as a microbial spray. The nucleotide sequences can be used alone or in combination to engineer microbes or other from Fronhials sinisfers. ö food 9, Crasta

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the patent discloses novel polynucleotides encoding Exophiala spinifera fumonisin degradative or transport enzymes such as flavin monocygenase, aldehydrogenase, permease and p-glycoprotein. A fumonisin esterase enzyme with at least one fermease and p-glycoprotein. A fumonisin esterase cargine and processing of the present in the action of a structurally related mycotoxin present in harvested grain, on application to a plant or to harvested grain of processed grain that is to be used as animal or human feed, or as a silage. Nucleotide fragments of the present invention are useful as processed grain era process and primers. They can be introduced into microorganisms that multiply on plants to deliver enzymes to potential target crops. The genes encoding the degrading enzymes are introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the pathogenicity of a fungus producing fumonisin. The genes of the invention are fermented in a bacterial host and the resulting bacteria is processed and used as a microbial spray. The nucleotide sequences or other organisms to metabolise fumonisin to engineer microbes or other organisms to metabolise fumonisin and resist its toxic effects.

The present sequence is a genomic DNA encoding Exophala spinifera
                                                                                                                                                                                                                                                                                                                        Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permease; p-glycoprotain; fumonisin esterase; adetoxification; mycotoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
attgotototatgagcagatetgtcaagagaaggtggccaattgggatgggtttgatgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR;
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                                                                                                                                                                                                                                                                                     Exophiala spinifera flavin monooxygenase genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1b; Page 63-64; 90pp; English.
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                                                          DNA; 1691
                                    1621 ettcatgotccctgctaa 1638
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P-PSDB; AAY72634.
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Mismatches
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Best Local Similarity
Matches 1184: Conserv
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RESULT 4
ABA15497/c
ID ABA15497 standard; DNA; 21100 BP.
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2000US-0231242
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14-AUG-2000;
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18-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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07-JUN-2000;
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                                                                                                                                                                                                                                                                         16-AUG-2001
                                                                  ABA15497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes the phytoene synthetase from Nicotiana tabacum. The phytoene synthetase coding sequence represents a cDNA of the invention. The isolated nucleic acid molecules are used for producing recombinant polypeptides or transgenic plants with enhanced ability to synthesise carotenoids. Phytoene has been used as ultra violet absorber and other carotenoids have been used as food colours, animal feeds and in the pharmaceutical and cosmetics industries.
                    1021 agcgactactacgaaatgctggacaagccgagcgtcgaaattgtgaatctagaacaatcg 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                      Phytoene synthase; transgenic plant; enhanced carotenoid synthesis; ultra violet absorber; food colour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding tobacco phytoene synthase polypeptides - useful for producing recombinant polypeptides or transgenic plants
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Pred. No. 21;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grill LK, Hellmann GM;
                                                              Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;
                                                                                                                                                                                                                Phytoene synthase coding sequence from N. tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 33-36; 25pp; English.
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363..1595
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Kumagai MH;
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                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                    AAV03881;
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibactrial; vulnerary; antiparkinsonian; antisickling; antianamato; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antianelergic; antidiabetic; antilucer; anticonvulsant; antiparasitic; cardiant; immune disorder; cardiancsular disorder; cardiant; immune disorder; cardiancsular disorder; deurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                    Human nervous system related polynucleotide SEQ ID NO 7828.
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(first entry)
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08-SEP-2000; 2000US-0231243,

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antigonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone and ovarian cancer and other cancers of the adrenal gland, bone, bone and user and sorders e.g. Addison's disease, allergies, autoimmune (b) immune disorders e.g. Addison's disease, allergies, autoimmune colitis; (c) cardiovascular olisorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal on the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
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Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF86431 standard; DNA; 349980 BP.
                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.2%; Soc
Best Local Similarity 100.0%; Pi
Matches 19; Conservative 0;
17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249390.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0251160.
05-DEC-2000; 2000US-0251160.
05-DEC-2000; 2000US-0251186.
06-DEC-2000; 2000US-02511866.
06-DEC-2000; 2000US-02511866.
08-DEC-2000; 2000US-02511869.
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Hyperthermophilic archaeon; hyperthermophilic protein; ds.

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15-OCT-1999;
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ID AAZ6
XX
AC AAZ6
XX
OT 23-M
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QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. the proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade.

110 degrees centigrade.

120 degrees centigrade.

131 degrees destigrade.

142 degrees sequences as shown in AAB99132-AAB99143, which AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag. EST. probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulocrary; antiparkinsonian; antiviral; csteopathic; neuroprotective; noctropic; antiparkinsonian; eserbroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluman; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
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                                                                                                                                                                                                                                                                                                                                                                                  New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry \boldsymbol{\cdot}
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Pred. No. 22;
0; Mismatches
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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100.0%; Pre
0;
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                                                                                                     AAH41223"
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Best Local Similarity
Matches 19; Conservat
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            Pyrococcus abyssi.
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Querellou J,
                                                        misc_feature
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AAA41261 to AAA43419 represent specifically claimed secreted expressed sequence tags (8ESTs), isolated from humen, mouse, xenopus and rat issues sources. The segre an have a range of activities depending on the Lissues they were isolated from. The activities depending on the Lissues they were isolated from. The activities include: chemokinetic; analgasic; hemostatic; thrombolytic; antifidations in the activities include: chemokinetic; antibacterial; antifidingal; antifivital; antifidabetic; antiparkinsonian; antificatic; antiparkinsonian; antiparkinsonian; antiparkinsonian; antiparcial cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene introduction and isolation of full-length copyas and genomic DNA molecules which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and ralising are useful; in assays for determining biological activity and ralising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (altheimer's, parkinson's, Huntington's disease, stroke), coagulation disease), tumours, bacterial, fungal or viral infections, depression and slasses), tumours, bacterial, fungal or viral infections, depression and seases). AAA4420 to AAA4420 repressent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polynucleotides, and encoded proteins, comprising secreted expenses expressed sequence tags (sESTs), useful for treating various disorders such as autofamune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; cosgulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psorlasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LaVallie ER, Collins-Racie LA, Evans C;
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v 100.0%; Pred. No. v..
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Best Local Similarity 100.0
Matches 18; Conservative
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Merberg D, Treacy M;
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us-09-882-694a-2.rng

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RESULT

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AA265250 to AA265350 represent 97 isolated human secreted protein genes.
This sequence was found to be present on human chromosome 1.

AAY76124 to AAY7623 represent the secreted proteins encoded by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions.

C. 9. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the mount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developmental abnormalities and foctal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, xidney disorders, atherosclerosis, diabetes, cardiovascular disorders, xidney disorders, atherosclerosis, diabetes, cardiovascular disorders, xidney disorders, and seedul for identifying their binding partners.

The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                 Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immines system disorder; inflammation; autoimmune disease; allery; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AlDS; leukaemia; therapy; chromosome 1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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Wei F, Brewer LA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1100 BP; 336 A; 197 C; 224 G; 343 T; 0 other;
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Olsen HS, Shi Y, Young PE, Wel E
Lafleur DW, Endress GA, Ebner R;
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  Human secreted protein gene 52.
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98US-0085094.
98US-0085105.
98US-0085906.
98US-0085920.
98US-0085921.
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98US-0085928
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P-PSDB; AAY76175.
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                                                                                                                                                                                         Homo sapiens.
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18-MAY-1998;
18-MAY-1998;
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12-MAY-1998;
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18-MAY-1998;
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The DNA (AAT07301) encoding the mature form of a collagenolytic type matrix metalloprofeease (MMP-1) (AAR87016) was isolated and adapted for expression in plants by addition of a start codon and a patatin leader sequence. The MMP construct (PAT COL) in vector Bin 19 was used to transform Agrobacterium GV 2260 and introduced into potato cv. Desiree and Maris Piper plants. The transgence plants showed high levels of resistance to the nematode Globodera pallida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid for increasing plant resistance to nematodes - encodes a polypeptide with collagenase activity.
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                                                                                                                    Type I matrix metalloprotease; MMP-1; collagenase; nematode; disease resistance; transgenic plant; crop improvement; nematocide; biological control; potato; Solanum tuberosum; ss.
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                                                                                            Type I matrix metalloprotease DNA
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             AAT07301 standard; DNA; 1110 BP.
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                                                                  19-MAR-1996 (first entry)
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es 18; Conservative
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                                        AAT07301;
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ABL20977/c
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AAT07301
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Gaps

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1.1%; Score 18; DB 21; Length 1100; 100.0%; Pred. No. 70; ive 0; Mismatches 0; Indels

Query Match 1.1 Best Local Similarity 100. Matches 18; Conservative us-09-882-694a-2.rng

Lu DAM;

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New human oxidoreductase proteins useful for diagnosing, treating or proventing proliferative, neurological, genetic, smooth muscle, autoimmune or infiammatory disorders associated with abnormal expression of oxidoreductase proteins
                                                                                                                                                                                                                                                              Claim 5; Page 89; 95pp; English.
                                                                                                                        Ive H, Tang YT, Baughn MR,
                           19-MAY-2000; 2000WO-US13879,
                                                     99US-0135049
                                                                                             (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                    WPI; 2001-025146/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 18; Conserv
                                                                                                                                                                 P-PSDB; AAB19927
                                                     20-MAY-1999;
27-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1130094-A2.
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 30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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ID AAK9
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drungs. The invention discloses genomic DNA sequences (ABLIGITS-ABL30511), expressed DNA sequences (ABL16175-ABL30511),
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB57737-ABB72072). This patent did not form part of the printed the specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OXRD-2; human; oxidoreductase; cell proliferation; neurological disease; amooth muscle disease; autoimmune disease; inflammation; antiproliferative; neuroprotective; immunosuppressive; antiinflammatory; gene therapy; diagnosis; ss.
Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 23; Length 1158; 70;
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 14404; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1158 BP; 252 A; 285 C; 329 G; 292 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human oxidoreductase OXRD-2 cDNA clone 1666030CB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.1%; Score 18; DB Local Similarity 100.0%; Pred. No. 70; Nes 18; Conservative 0; Mismatches
                                                                                                                                                                                                                        Myers EW;
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29..1318
/*tag= a
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                                                                                                                                                                                                                     Li PWD,
                                                                                                                        23-MAR-2001; 2001WO-US09231.
                                                                                                                                                23-MAR-2000; 2000US-191637P.
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                                      Drosophila melanogaster.
                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                               WPI; 2001-656860/75
                                                                                                                                                                                           (PEKE ) PE CORP NY.
                                                                 WO200171042-A2
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                                                                                                                                                                                                                                                                                                      interactions
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                                                                                             27-SEP-2001.
                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The present sequence is that of Incyte clone 1666030CB1 encoding human oxidoreductase OXRD-2 (see AAB19927). The gene maps to chromosome I between 278.8 and 292.7 or. The clone was isolated from human breast tissue colbA library BRSTMOTO9. The encoded protein shows homology to Plasmodium falciparum FAD-dependent oxidoreductase. OXRD-2 is expressed in nervous, reproductive and gastrointestinal tissue, and may be involved in cell proliferation and inflammation. The invention provides Norly proliferation of cast AAB1926-33) and polynucleotides (see AAB1926-92). It also provides methods for using these polypeptides and polynucleotides (see AAB19926-92). It also provides methods for using these polypeptides and polynucleotides associated with expression of OXRD, especially call proliferative, neurological, genetic, smooth muscle, and autoimmune/inflammatory disorders. A vector encoding OXRD or its fragments is useful for sometic or germine gene therapy for treating such disorders. The polynucleotides may also be used to monitor regulation of OXRD incledides and disorders. The prolectides and proper intervention. A DNA fragment comprising nucleotides 173-217 of the present sequence can be used as a hybridization probe.
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimmlant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialammatory; antianemic; gene therapy; cancer; proliferative discorder; ontifundatic; antithyrold; antianaemic; gene therapy; cancer; proliferative discorder; osteoarthritis; graft vs host disease; cardiovascular disease; disbetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autofimune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobiauria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaquiation;
                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIO1840-ABLIG175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed at fite.wipo.int/pub/published_pct_sequences.
detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                       Claim 1; SEQ ID NO 41747; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF2197 polynucleotide sequence SEQ ID NO:4393.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2095 BP; 607 A; 520 C; 517 G; 451 T; 0 other;
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Pred. No.
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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  New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.19
Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-602362/57.
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                                                  interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC76642;
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to primers for synthesising full length CDNA closes. 830 cDNA molecules encoding a human protest have been isolated and nuclectide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length constructed cDNA libraries that were synthesised by the Oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                             830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation .
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                                                                                                                                    ai T, Hayashi K, Ishii S, Kawai Y;
Nagai K, Kojima S, Otsuki T, Koga
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Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID NO 3398; 1380pp + sequence listing; English.
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                                                                                                                                  Ota T, Nishikawa T, Isogai T,
Wakamatsu A, Sugiyama T, Nagai
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Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
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     08-JUL-1999; 99JP-0194486,
11-JAN-2000; 2000JP-0118774,
02-MAY-2000; 2000JP-0183765.
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                                                                                          (HELI-) HELIX RES INST.
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                                                                                                                                                                                                WPI; 2001-524255/58.
P-PSDB; AAM93594.
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Gaps 6

Indels

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23; Length 2095;

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Adams M,
WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostafic; hepatotropic; vulnerary; antipactatic; anticonvulsant; antiarthritic; immunosuppressant; coteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; antidiabetic; hypotensive; deradiont; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; deradiont; antidiabetic; hypotensive; deradiont; antidiapetic; hypotensive; deradiont; coaquiant; vasotropic; antidiamatory; antibacterial; antivitary; antifinetumatic; antidiapetic; hypotensive; deradiont; descriptions associated with an ORFX associated disorder. The proteins and antianaemic which and open therapy vectors. The proteins associated with an ORFX associated disorder; vactors: The proteins and nucleic acids may be used to treat cancers, outled acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, cafer vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus corpusation, hypothyroidism, cholesterol esters storage, systemic lupus antergies, aplastic namenals, burns, wounds, bone and cartilage damage, cocurnal haemoglobinuria, antidiflammatory disease; to enhance conturned the conturned as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                       Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 18; DB 21; Length 2171;
100.0%; Pred. No. 70;
1ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2171 BP; 584 A; 429 C; 505 G; 653 T; 0 other;
                                                                             Claim 5; Page 3582-3583; 5507pp; English.
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27-ANG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776,
02-MAY-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.08
Matches 18; Conservative
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Ishii S,
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an ollogouchedetide complementary complementary primer and an ollogouchedetide complementary of the 5602 nucleotide sequences defined in the specification, where the collogoucleotide comprises at least 15 nucleotides; or (b) a combination of an ollogoucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an ollogoucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the ollogoucleotide which comprises a 3'-end sequence is allogoucleotides of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in suttaense therapy and can gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, and agnosts of the abnormality of the full-length cDNAs. The primers also useful for the convas easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 represent human annino acid sequences; and AAH13629 to AAH13632 represent human annino acid sequences; and AAH13639 to AAH13632 represent human annino acid sequences; and AAH13639 to AAH13632 represent human annino acid sequences; and AAH13639 to AAH13632 represent human annino acid sequences; and AAH13639 to AAH13631 processor.
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                        Claim 8; SEQ ID 16700; 2537pp + CD ROM; English.
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00.0%; Pred. No. 70;
ve 0; Mismatches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0167-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB97137-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                   Claim 1; SEQ ID NO 14401; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3158 BP; 875 A; 749 C; 697 G; 837 T; 0 other;
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Search completed: April 27, 2002, 05:28:04 Job time: 13767 sec

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Gaps ô

Query Match 1.1%; Score 18; DB 23; Length 3158; Best Local Similarity 100.0%; Pred. No. 70; Matches 18; Conservative 0; Mismatches 0; Indels

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4.5 Compugen Ltd.		Search time 7820.58 Seconds (without alignments) 4383.008 Million cell updates/sec	cta		sən	s: 3595312			· · ·		U	35	0			1 4 4 4		RESULT AXO76843	DEFINITION	VERSION	SOURCE		REFERENCE	ave a g printed,	PEATURES	
GenCore version 4.5 Copyright (c) 1993 - 2000 Con	OM nucleic - aucleic search, using sw model	Run on: April 27, 2002, 00:46:03 ; Sear (V 43	Title: US-09-882-694A-2 Perfect score: 1638 Sequence: 1 atgtcggccaccagcaactc	able: OI	shed:	Word \$126 : 0 Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	Database : GenEmbl:*	; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;		5: gb_ov:* 6: gb_pat:*	7: gb_ph;* 8: qb_pl;*	9: 95 pr:* 10: 9b pr:*	11: gb.sts:* 12: gb.sts:*	13: 9b_vi:* 14: 9b_vi:* 15: em_ba:*	16: em_fun:* 17: em_hum:* 18: em_in:*	21: em_or:* 22: em_ov:* 23: em_ov:*				30: em_htg_lnm:* 31: em_htg_inv:* 32: em htg rther:*		Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.	SIDMABIES	- Ac

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Exophiala spinifera.

Exophiala spinifera

Exophiala spinifera

Eukaryota; Fungiliana

Chaetothyriales; Herpotrichialaceae; mitosporic

Herpotrichialaceae; Exophiala.

(basea I to 1691)

Duvick, J.P., Maddox, J., Gilliam, J., Folkerts, O. and Crasta, O.R.

Compositions and methods for fumonisin detoxification

Patent: WO 0105980-A I 25-JAN-2001;

Pioneer Hi-Bred International Inc. (US); Curagen Corporation (US)

Location/Qualifiers
                                                                                                                                                                                                                                                                        GATCTCATGGCTCCTCTGGAGCCGCCGTACTGGTTCGGTACCAAGCGCTCCCCACTGGAG
              trgaaaaacaagcacggagtggacctgaaggaggtgtgtggaaagatggcatatctacttat
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/db_xref="taxon:91928"
/note="flavin monoxygenase with intron"
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Sequence 1 from Patent W00105980.
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                   Score 1638; 1
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22-FEB-2001

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2 (bases to 6047)

Tavakoli,N.
Direct Submission

Direct Submission

Direct Submission

Direct Submitted (01-NV)-1994) N. Tavakoli, University of Bristol, Dept of Pathology & Microbiology, The Medical School, University Walk, Bristol BSS 1TD, UK

Revised by [3]
                                                                                                                                                                                                                                                    1 (bases 1 to 6047)
Tavakoli,N.P., Comanducci,A., Dodd,H. and Bennett,P.M.
pUBJ380 carries a putative transposable element (IS1294) capable emplaiting one-ended transposition
Unpublished
                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                /note="confers kanamycin resistance, aminoglycoside 3/
phosphotransferase type 1"
2249. .3064
Tavakoli, N.
Direct Submission
Submitted (15-JUL-1997) N. Tavakoli, University of Bristol, Del Pathology & Microbiology, The Medical School, University Walk, Bristol BSB 1TD, UK
On Apr 25, 1998 this sequence version replaced gi:572684.
                                                                                                                                                                                                 aminoglycoside 3'-phosphotransferase; aph gene; transposable
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1.8;
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/note="origin of replication region"
1333 c 1448 g 1726 t 3 o
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/organism-"Escherichia coli"
/plasmid-"pUB2380"
/strain-"SE53"
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                                                                                                                                                     E.coli transposable element IS1294.
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/gene-"tnp1294"
/gene-"tnp1294"
/gene-"tnp1294"
/note-"transposase"
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   Length 1691;
                        Indels
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  DB 6;
 72.3%; Score 1184; D
100.0%; Pred. No. 0;
ive 0; Mismatches
          Best Local Similarity 100.
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Richaess 1 to 29716)

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Richaess 2 (bases 1 to 20716)

Richaess 3 to 20716

Richaess 3 to 20716

Richaess 3 to 20716

Rooke, 1 Canarata, 2 Canarata, 3 Cook, A. Chang, 3. Changelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Erizellano, K., Dewar, K., Diaz, J., Sarogue, S., Faro, S., Faro, S., Faro, S., Faro, S., Goyette, M., Graham, L., Garad-Pierre, N., Glode, S., Goyette, M., Graham, L., Garad-Pierre, N., Jones, C., Kamat, A., Kalls, C., Levine, R., Maldrim, J., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Connor, T., O'Donnell, P., Peterson, R., Sahoe, R., Stange-Thomann, N., Stojanovic, N., Stange, Thomann, J., Zambek, L., Zhmmer, A., and Zody, M.

All repeats were identified using Repeatwasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Center Conter Explantation Center For Center Fores were identified using Repeatwasker.html
                                AC103823 29716 bp DNA linear HTG 29-NOV-2001
HOMO Saplens chromosome 8 clone CTD-2121K3 map 8, LOW-PASS SEQUENCE
SAMPLING.
                                                                                                                                                                                                                                                                    Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 29716)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens Armonsome 8, clone CTD-2121K3

Unpublished
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
sarbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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700 799: gap of 100 bp

800 1502: contig of 703 bp in length

1503 1602: gap of 100 bp

1603 2296: contig of 694 bp in length

2377 2396: gap of 100 bp

2377 3101: contig of 705 bp in length

3102 3201: gap of 100 bp
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Center clone name: 2121_K_3
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HTG; HTGS_PHASE0.
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RESULT 5
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KEYWORDS
SOURCE
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Homosaplens
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa: Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 63585)

Bliren B., Linton, L., Nusbaum, C. and Lander, E.

Homo saplens chromosome B, clone RP11-37673

AL Unpublished

E (bases 1 to 63585)

Bliren B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

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Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

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Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collins, S.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Helon, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J.,

Kielin, J., Meneus, L., Milver, J., Macdonald, P., Morrow, J.,

McCarthy, M., McEwan, P., McGurk, A., McRernan, K., McPheeters, K.,

Collymor, Santos, R., Schauer, S., Sovery, P., Spencer, B.,

Stange-Thomann, N., Stojanoric, N., Subramanlan, A., Talamas, J.,

Young, G., Zahnoun, J., Zimmer, A., Travers, M., Trigillo, J.,

Voung, G., Zahnoun, J., Zimmer, A., Travers, M., Trigillo, J.,

Direct Subalssion, Conv., Linter, L., Lander, C., Converter, M.,

Collymore, M., Subalson, P., Welley, M., 
                                                                                                                                                                                                                                                                       63585 bp DNA 11near HTG 25-MAR-2000
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ACC26983.1 GI:7328861
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
Length 29716;
                                                                    0; Indels
      DB 2;
   Query Match 1.2%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 23; Matches 20; Conservative 0; Mismatches
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                                                                                                                          Center project name:
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AC026983/c
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KEYWORDS
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TITLE
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AUTHORS
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11572 1245: contig of 838 bp in length 11572 12465: contig of 894 bp in length 12466 12565: gap of 100 bp 12566 13397: contig of 832 bp in length 1358 13497: gap of 100 bp 13398 13497: gap of 100 bp 14354 14453: gap of 100 bp 14354 14453: gap of 100 bp 14454 15274: contig of 856 bp in length 14354 14453: gap of 100 bp 15375 15374: gap of 100 bp 16375 1720: contig of 872 bp in length 1637 1720: contig of 885 bp in length 17202 17301: gap of 100 bp 18190 18299: gap of 100 bp 18190 18299: gap of 100 bp 18190 18299: gap of 100 bp 18190 18290: gap of 100 bp 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18290 18
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             the accession number will
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30817: contig of 853 bp in length
30917: gap of 100 bp
31801: contig of 884 bp in length
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27904; contig of 885 bp in length
28004; gap of 100 bp
28888; contig of 884 bp in length
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31902 32742: contig of 841 bp in length
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839 938: gap of 100 bp
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29864: contig of 876 bp in length
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11471: contig of 858 bp in length
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e record is updated, preserved.
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7596
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Gaps ö Length 63585; 25 34824; gap of 100 bp 35595; contig of 871 bp in length 5756; gap of 100 bp in length 100 bp 3765; gap of 100 bp in length 100 bp 38571; contig of 893 bp in length 38571; contig of 893 bp in length 100 bp 38571; contig of 893 bp in length 100 bp 38571; contig of 893 bp in length 100 bp 38571; gap of 100 bp 58779 58818: gap of 58879 58879 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 58870 5887 0; Indels Query Match 1.2%; Score 20; DB 2; Best Local Similarity 100.0%; Pred. No. 22; Matches 20; Conservative 0; Mismatches ( /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="8" /map="8" /clone="RP11-376P3" Location/Qualifiers source FEATURES ò

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Birren B. Linton'L., Nusbaum,C., Lander E., Abraham,H., Allen,N., Anderson,S., Baldwin, Beckerly,R., Beda,F., Cooke,P., Chopel, I., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Chopel, I., Colangelo,M., Devile,M., Ferestor,J., Cooke,P., Chopel, I., Colangelo,M., Devile,M., Ferestor,J., Cooke,P., Denarellano,R., Demark, C., Gago,D., Galagan,J., Cardyna,S., Callymore,A., Cooke,P., Cardyna,S., Callymore,A., Mckenna,G., Cardyna,S., Callymore,A., Mchan,J., Cardyna,S., Callymore,M., Retastor,J., Marchis,J., Morrow,J., Naylor,J., Landers,T., Lehoczky,J., Levine,R., Heaford,A., McKernan,R., Macdonald,P., Marquis,N., McEwan,P., McGrick,A., McKernan,R., McPherers,R., Meldrin,J., Menesis,L., Morrow,J., Naylor,J., Norman,C.H., Coonor,T., O'Donnell,P., Ollvar,T.H., Peterson,R., Severy,P., Subreamian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassillav,H., Viel,R., Yo,A., Wu,X., Wyman,D., Ye,W.J., Illaw,J., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Tilmer,A. and Zody,M.

Limmer,A. and Zody,M.

Bayes,B., Lo 149179,

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Cooke,P., Dearellano,R., Daga,Lav,Yy, L., Boukhgalter,B., Bruwn,A., Camarata,J., Campoplano,A., Changellano,R., Dada,S., Collymore,A., Boyetter,M., Changellano,R., Dada,J.S., Dodge,S., Barre,M.

Reperson,S., Barra,M. Bastlen,V., Boyatlavky,L., Bodde,S., Gord,S., Cooke,R., Diaz,J.S., Dodge,S., Rayer,M.

Rodes,C., Kamat,A., Kantas,A. Kells,C., Lakocque,K., Matches,R., Malley,B., McKernan,R., Menes,C., Manderson,R., Manderson,R., Manderson,R., Manderson,R., Manderson,R., Manderson,R., Stencer,B., Stencer,B., Stencer,B., Stencer,B., Stencer,B., Stencer,B., Stencer,S., Stencer,S., Stencer,S., Stencer,B., Stencer,B., Stencer,B., Stencer,B., Stencer,B., Stencer,
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Hirdon, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Choppel, Y., Camareta, J., Campoplano, A., Chang, J., Chazaro, B., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149179)
                                                                                                                                                    149179 bp DNA linear Homo saplens, clone RP11-24F3, complete sequence. AC021694.8 GI:17488694
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens, clone RP11-24F3
Unpublished
Young, G., Zalnoun,
Direct Submission
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                                                                                                                                                                                                                                                                                                                             human.
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 95623 bases at least Q40
Consensus quality: 97794 bases at least Q30
Consensus quality: 97794 bases at least Q30
Consensus quality: 9843 bases at least Q30
Consensus quality: 98743 bases at least Q20
Estimated insert size: 75000; agarose-fp estimation
Betimated insert size: 97715; sum-of-contigs estimation
Quality coverage: 4.94 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                     ACUSTA/O 99015 bp DNA linear HTG 31-AUG-2001 HOMO Sapiens chromosome 5 clone CTD-2385B5, WORKING DRAFT SEQUENCE, a unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
1 (bases 1 to 99015)
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1.2%; Score 20; DB 2; Length 99015;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
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Db 36649 GCCTTCCCCAATGCCTTCTT 36630
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AC024978
Location/Qualifiers
1. 149179
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123. 179
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7510. .7606
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4361.4487
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52630.5261
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Gaps ö DB 9; Length 149179; 21; 0; Indels / 13976 / 13976 / 19976 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 / 1992 /rpt\_family-"THEIB-int"
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016148 106247; contry of 2471 pp in tength
106248 133039; contry of 26792 bp in length
133040 133139; gap of 100 bp
133140 135781; contry of 25642 bp in length.
Location/Qualifiers
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62414: contig of 16088 bp in length
                                                                                                    contig of 1468 bp in length of 100 bp contig of 2519 bp in length contig of 2519 bp in length
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contig of 1572 bp in length
of 100 bp
contig of 1136 bp in length
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11644; contig of 2259 bp in length
11744; gap of 100 bp
14644; contig of 2900 bp in length
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6666: con
6: gap of
9285: con
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Unpub
AC024978 158781 bp DNA linear HTG 26-MAY-2000 Homo sapiens chromosome 16 clone RP11-285K4 map 16, WORKING DRAFT SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center clone name: 1289_K_4
Center clone name: 1289_K_4
Center clone name: 1289_K_4
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator High Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 146857 bases at least Q40
Consensus quality: 146886 bases at least Q30
Consensus quality: 154688 bases at least Q30
Consensus quality: Sum-of-contigs
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 16, clone RP11-285K4 Unpublished
                                                                                                                                                        AC024978.3 GI:8076921
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pherre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schubback,R.,
Sewery,P., Spencer,B., Stange-Thomann,M., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tophan,K., Travers,M., Travis,N., Trigilio,J., Vassillev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Losenthies Street, Cambridge, MA 02141, USA
On Oct 11, 2001 this sequence version replaced gi:15148331.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fep.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center: sequence_submissions@genome.wi.mit.edu
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Signates, I. Litton, J., Nusbaun, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Conjuno, A., Carlette, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodges, J., Danino, M., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Kiein, J., LaRocque, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKenan, K., Mordow, T., O'Donnell, P., McGarthy, M., McEwan, P., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Waylor, J., Norman, C.H., O'Connor, P., O'Donnell, P., O'Nell, D., Ollyar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., And D2141, USA
B. Santses Street, Cambridge, MA 02141, USA
B. Santses Street, Cambridge, MA 02141, USA
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Homo sapiens chromosome 8, clone RP11-234A3, complete sequence.
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Mammalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                            Query Match 1.2%; Score 20; DB 2; Length 158781; Best Local Similarity 100.0%; Pred. No. 20; Matches 20; Conservative 0; Mismatches 0; Indels 0.
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Home saplens appleas the translate; Vertebrate; Euteleostomi; Bukaryote; Metazoa; Chordate; Craniata; Vertebrate; Euteleostomi; Eukaryote; Metazoa; Chordate; Craniata; Euteleostomi; Eukaryote; Linton.L., Nusbaum,C. and Lander,E.

1 (bases 1 to 162054)

AL Salaren, E., Linton,L., Nusbaum,C., Lander,E., Abreham,H., Allen,N., Anderson,S. Baldun,J., Barna,N., Bastlen,V., Beda,F., Boduslavkiy,L., Boukhigalter,B., Brown,A., Burket,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diax,J.S., Dodge,S., Domino,M., Oyle,M., Ferreire,P., Fitzhugh,M., Gage,D., Grand Pierre,N., Grand,G., Hagos,B., Hedelord,A., Horton,L., Rarata, Hedelord,A., Grand,G., Hagos,B., Hedelord,A., Horton,L., Rarata, Hedelord,A., Grand,G., Hagos,B., Hedelord,A., Horton,L., Howland,J.C., Iliav,I., Jamazares,R., Landers,T., Lehoczky,J., Howland,J.C., Iliav,I., Jamazares,R., Landers,T., Lehoczky,J., Howland,J.C., Iliav,I., Mangav,H., McKenan,R., McKe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC046201 162054 bp DNA linear HTG 12-MAY-2000 Homo sapiens chromosome 17 clone RP11-199J4 map 17, WORKING DRAFT SEQUENCE, 35 unordered pieces.
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: L9710t
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Center clone name: 199_1_4
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Consensus quality: 181600 bases at least 030
Consensus quality: 181630 bases at least 030
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Homo sapiens
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Outlify coverage: 3.1 in 020 bases; sum-of-contigs
In of known and thair order in this sequence record as
any consists of 35 contigs. The true order of the pieces
In of known and thair order in this sequence record as
any conting of 131 bp in length
I192 1491; app of 100 bp in length
I192 1491; app of 100 bp in length
I193 1491; app of 10
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110783 110882: gap of 100 bp
110883 120476: contig of 9594 bp in length
120477 120576: gap of 100 bp
133126 13225: contig of 11549 bp in length
133126 13225: gap of 100 bp
133226 14566: contig of 13435 bp in length
14561 145760: gap of 100 bp
14571 15054: contig of 16294 bp in length.
Location/Qualifiers
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5395. .6549
Anote—"assembly_fragment"
6560. .8183
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Jase. 38785
Jase. 38785
Jace. 43323
Jace. 43323
Jallo. 46470
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Gaps

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HTG; HTGS_PHASE1; HTGS_DRAFT.
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AC079184/c
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Unpubl
                                                                                                                                                                                                                     AC091097 162515 bp DNA linear HTG 09-FEB-2002 Homo sapiens chromosome 11 clone RP11-65C9 map 11, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo saplens
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162915)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-65C9
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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* Location/Qualifiers
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Web Site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@senome.wi.mit.edu
Contact: project information
Center project name: Li1779
Center clone name: 65_C_9
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HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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DEFINITION
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Homo saplens Bukaroa; chordata; Cranlata; Vertebrata; Euteleostoml; Bukaryota; Metazoa; chordata; Catarrhini; Hominidae; Homo.

E Jobases I to 163453)

Bitren B. Linton.L., Nusbaum.C. and Lander.E. Abraham,H., Allen,N., Butren.B., Linton.L., Nusbaum.C. and Lander.E. Abraham,H., Allen,N., Butren.B., Linton.L., Nusbaum.C., Lander.E., Abraham,H., Allen,N., Butren.B., Linton.L., Burket.G., Campoplano.A., Castle, Chospel.Y., Colangelo,M., Collins,S., Collins,S., Gorder,E., Chospel.Y., Colangelo,M., Castle,N., Chospel.Y., Colangelo,M., Castle,N., DeArellano.R., DeWar, Castle,N., DeArellano.R., DeWar, Castle,N., DeArellano.R., DeWar, M., Marchan,L., Grand Plerren.N., Hagos,B., Hagford,A., Horton.L., Lamazares.R., Landers,T., Lehoczky,J., Earcelta,P., Lamazares.R., Landers,T., Lehoczky,J., Hafford,A., Horton.L., Lamazares.R., Landers,T., Lehoczky,J., Hafford,A., Horton.L., Lamazares.R., Handry,M., Castle,M., McCarthy,M., McCannor,T., Marquis.N., McCarthy,M., McCannor,T., Marquis.N., McCarthy,M., McCannor,T., Marquis.N., McCarthy,M., McCannor,T., Connor,T., Marquis.N., McCarthy,M., Calling,P., Polinar,V., Sander,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,M., Stolanovic,N., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,M., Stolanovic,N., Threell,A., Trrell,A., Travers,M., Trigilio,J., Vassillev,H., Viel,R., Vo.A., Threell,A., Trevers,M., Trigilio,J., Vassillev,H., Viel,R., Viel,R., Submitted (23-AuG-2000) Whitehead Institute/MIT Center for Genome Canter Cambridge, MA 02141, USA On Jan 15, 2001 this sequence Version replaced giig86020.

All repeats were identified using RepeatMasker: html
Center claumisty Statistics
Smalt, A. R. A. & Green, P. (1996-1997)
http://ftp.genome.washigton.edu/RM/RepeatMasker: html
Center sequence_Submissions@genome.Wimit.edu
Center sequence_Submissions@genome.Wimit.edu
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Center sequence_Submissions@genome.Wimit.edu
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Center sequence_Submissions
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Homo saptens chromosome B clone RP11-296E5 map B, WORKING DRAFT
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Query Match
1.2%; Score 20; DB 2; Length 162515;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0.
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Waterson, R. H.
The sequence of Homo sapiens clone
Uppublished
1 (bases 1 to 164436)
Waterston, R. H.
Direct Submisser Submisson
Submitted (15-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                           ACUDIDES 1164436 bp DNA 11near HTG 01-SEP-2000 Home sapiens chromosome 11 clone RP11-65C9, WORKING DRAFT SEQUENCE, ACKING PIECES.
                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaliai: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164436)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is rubitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WuGSC
Web Site: http://genome.wustl.edu/gsc/index.shtml
Web Site: http://genome.wustl.edu/gsc/index.shtml
Center code: WuGSC
Center project name: H NNO05609
Center project name: H NNO05609
Sequencing vector: M13: 100%
Sequencing vector: M13: No of reads
Centering vector: M13: No of reads
Sequencing vector: M13: No of reads
Chemistry: Dye-primer E7: 100% of reads
Assembly program: Phrap: version 0.99019
Consensus quality: 156732 bases at least Q20
Consensus quality: 156732 bases at least Q20
Insert size: 16100: agarose-fp
Insert size: 16100: agarose-fp
Insert size: 16307; sum-of-contigs
Quality coverage: 3.7% in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
length
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bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 1489 bp in lengapo ou unknown length
gap of unknown length
contig of 1897 bp in lengapo of unknown length
contig of 1763 bp in lengapo of unknown length
contig of 1716 bp in lengapo of unknown length
contig of 1633 bp in lengapo of unknown length
contig of 1513 bp in lengapo ou nknown length
contig of 1813 bp in lengapo of unknown length
contig of 1818 bp in lengapo of unknown length
contig of 3018 bp in lengapo of unknown length
contig of 3018 bp in lengapo of unknown length
contig of 3645 bp in lengapo of unknown length
                                                                                                                                                            AC051656
AC051656.3 GI:9838050
HTG; HTGS_PHASE1; HTGS_DRAFT.
Db 130687 rccaGarrGrrcaGGAGTrG 130668
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7107:
7207:
8923:
9023:
10656:
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15389:
15489:
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1590
3248
3348
5245
5345
7108
7208
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10657
10757
12272
12372
15390
15490
                                                                                                                                                                                                                            human.
                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                           RESULT 14
AC051656
                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                       MOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as its available and the accession number will be preserved.
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                                                      Insert size: 16300; agarose fp
Insert size: 16365; sum-of-conlitys
Quality coverage: 5.7 in Q20 bases; sum-of-conlitys
Quality coverage: 5.7 in Q20 bases; sum-of-conlitys
                                                                                                                                                                                                                                                                                                                                                                                                                                801 others
                                                                                                                                                                                                                                                                                                                                                    9660 9759; gap of 100 bp

9760 10810: contig of 1051 bp in length

10811 10910; gap of 100 bp

10911 14021: contig of 3111 bp in length
Consensus quality: 160037 bases at least Q40 Consensus quality: 161862 bases at least Q30 Consensus quality: 162334 bases at least Q20
                                                                                                                                                                                                                                                                                                                                    9659: contig of 9659 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-296E5"
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52229 a 30041 c 28914 g 51467 t
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700...1021

700...14021

700...14021

700...19568

14.122...19568

14.122...19569

700...25031

700...25031

700...25031

700...3359mbly_fragment

31560...38459

700...3858mbly_fragment

31560...38459

700...3858mbly_fragment

31560...3858mbly_fragment

700...38963...32447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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25047: contig of 3245 bp in length
25047: contig of 4726 bp in length
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42941: contig of 7078 bp in length
42941: contig of 7078 bp in length
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73293: gap of unknown length
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81380: contig of 7841 bp in length
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115888: gap of unknown length
118883: contig of 12788 bp in length
128803: contig of 12788 bp in length
128803: contig of 12788 bp in length
128803: contig of 13788 bp in length
128803: contig of 53533 bp in length
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7note="assembly_name:Contigl4"
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22902 ...
7note="assembly_name:Contigl5"
23003 ...26247 ...
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contig
gap of
contig
gap of
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gap of
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Direct Submission

In Submitted (10-Jan-2001) Production Sequencing Facility, DOE Joint
Submitted (10-Jan-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

So Doint Genome Institute

Direct Submission

L Submitted (10-Far-2002) Production Sequencing Facility, DOE Joint
Submitted (10-Far-2002) Production Sequencing Facility, DOE Joint
Cenome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 4, 2002 this sequence version replaced gi:15963645.

Sequence Quality has been annotated with sequence quality
estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
I error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are evaliable as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACUB/365 192974 bp DNA linear PRI 04-FEB-2002 Homo saplens chromosome 16 clone RP11-53L24, complete sequence. ACOB/365
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Bunmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 192974)
DOG Johit Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Quality Assessment:

This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 164436; 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2313 others
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DOE Joint Genome Institute.
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DEFINITION
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ORIGIN
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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FEATURES LOCATION/Qualifiers
source 1.192974
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/ Ab\_xref="taxon:9606" |
/ Chromosome="16" |
/ Chromesome="16" |
/ Clone="RPI1-53124" |
BASE COUNT 57606 a 41225 c 39814 g 54329 t

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0;

Search completed: April 27, 2002, 05:23:55 Job time: 16672 sec

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us-09-882-694a-11, rspt

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April 27, 2002, 07:57:47; search time 114.27 Seconds (without alignments) 1912.073 Million cell updates/sec
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6455
1 MADESEKPRPNQDGSESSSH......LQRLRGRYYEWCLAQSLDQA 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562222
GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                         OM protein - protein search, using sw model
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1: Sp_Barchea!:*

2: Sp_Barchea!:*

4: Sp_Barchea!:*

5: Sp_Inng1:*

6: Sp_Innannal:*

7: Sp_Inc:*

8: Sp_Inc:*

9: Sp_Ind:*

1: Sp_Ind:*

1: Sp_Ind:*

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5: Sp_Ind:*

5: Sp_Ind:*

6: Sp_Inc:*

7: Sp_Ind:*

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8: Sp_I
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q9y8g2 emericella Q9y8g1 emericella	09hqt5 trichophyto 099748 emericella 043131 second 110	O43140 aspendinus O43140 cryptococcu O43138 asperqillus	093437 gallus gall Q91586 xenopus lae	046605 canis famil 002793 ovis aries	Q9jk64 rattus norv Q92416 rattus norv	O45721 caenorhabdi Q9m1q9 arabidopsis Q9fwx7 arabidopsis
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                                                                                             Indels 104; Gaps
                                                                                                                                                                       7 KPRPNQDGSESS----SHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGAS 62
                                                                                                                                                                                                                                  DLPREKQMELVQKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDP
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tch 36.8%; Score 2378; DB 3; al Similarity 40.1%; Pred. No. 1.1e-152; 528; Conservative 233; Mismatches 453;
         Ouery Match
Best Local S.
Matches 528
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980 TSFTKARSAANYILWLRTLKPTIRETEENKKKGPVGGCPVDLEDIEFRYRQRDSARVLRG 1039
                                                                                                                              1100 VQQEPTLYQGSVRENVTLAL------EAELSEELCQGRLPARPMLWILSSLY 1145
                                                                                                                                                                                                                                                                                                                                   1108 VQQEPTLFQGTIRDNISLGVFNPNTQPFFSDKDAVKSVSDEQIESALRAANAWDFVSSLP 1167
                                                                                                                                                                                                                                                                                                      1146 OKALKRLAAORGMOFSGGORQRIAIARALIRNPKLLLLDEATSALDTGSERLVQAALDEA 1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ADESEKPRPNODGSESS-----SHPPPE-----KETEGSISDYLRIFRYADKY 44
                             .040 VSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATRD OR ABCD.

Beneficella nidulans (Aspergillus nidulans).

Eukaryota: Fungi, Ascomycota: Pezizomycotina; Eurotiomycetes;

Eurotiales: Trichocomaceae; Emericella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrade A.;
"Two novel ABC transporters from Emericella nidulans.";
submitted (JUN-1998) to the EMBL/GenBank/POBD databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN MDR (ABC-TRANSPORTER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.0%; Score 2001; DB 3; Best Local Similarity 37.5%; Pred. No. 4.8e-127; Matches 500; Conservative 230; Mismatches 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR003593; AAA.
InterPro: IPR00140; ABC_transporter_tmem.
InterPro: IPR001499; ABC_transportr.
InterPro: IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00065; ABC_tran; 2.
SMART; SM00382; AAA; 2.
PROSITE: PS00211; ABC_TRANSPORTER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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ATP-binding; Transport.
SEQUENCE 1348 AA; 1A
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDIFRFFVCFS-EILFGAQSAGTVFSFAPDMGKAKNAAAEFRRLFDRKPQIDNWSEEGEK 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 KGPVGGCPVDLEDIEFRYRQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERF 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLAL-EAELSEE-LC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASFNRPEIPY-MLIGLVFSVLAGGGQPTQAVLYAKAISTLSLPESQYSKLRHDADFWSLM 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALPTQLQEL------ISANFLIYIVVGQHRLEQC-STISLWMETGPGGCVW 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STETKHLSGVSGVTLGTILMTSTTLGAAIIIALAIGWKLALVCISVVPVLLACG----- 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGH 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 ---FYRFYMLAOFQSRS----KLAYEGSANFACEATS---SIRTVASLIRERDVWEIYH 989
                                                                                                                                                                            : :|: | | || | | :| | || || :| || HEGLMYSNYGLGFWMGSRFLVDGAV-DVGDILTVLMAILIGSFSLGNYSPNAQAFTNAVA 411
                                                                                                                                                                                                                          :::| ||: ; ||| || ; || || 412 AAAKIEGTIDRQSPLDPYSNEGKTLDHFEGHIELRNVKHIYPSRPEVTVMEDVSLSMPAG 471
                                                                                                                                                                                                                                                                                                       RGTIFQNIANGFMDEQRDLPRE-KQMELVQKACKASNGDVFINELPNGYETEVGERAGAL 523
                                                                                                                                                                                                                                                                                                                       SGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLAT 583
                                                                                                                                                                                                                                                                                                                                                                    -----KTLHEKAAREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCI-LI 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADIAKIKTA-SSASSDLDGKPTTIDRTGTHKSVSSAILSKRP-PETTPKYSLWTLLKFV 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLHTVFEL---SGHAAQERADFYILM 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQL 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VE---QG---LAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLN--- 957
DILIMVISTICAIAAGAALPLFTILFGSLASTFQRIMLYQISYDEFYDELTKNVLYFVYL 172
                      FIGKFVLTYVSTAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNR 164
                                                                                         IQDGISEKVGLTLTALATFVTAFIIAYVKYWKLALICSSTIVALVLTMGGGSQFIIKYSK 292
                                                                                                                                                              EYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRI 344
                                                                                                                                                                                                            FGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAG 404
                                                                                                                                                                                                                                                        KTTALVGASGSGKSTMVGLLERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLF 464
                                                                                                               RITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFST
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| 11 | PERCHANGE FROM N.A. | A RECCHETORI W. Jr., | A RECLIN A.L., FERTEIR - NOZZWA M.S., MACCHETORI W. Jr., | PERCHING A.L., FERTEIR - NOZZWA M.S., MACCHETORI W. Jr., | MATLINEZ-ROSSI N.M.; | TIGHILIGATION and Characterization of atrD gene, a new multidrug TATP-Blanding Cassette Transporter of Trichophyton rubrum."; | Submitted (AdC-2001) to the EMBL/GenBank/DbBJ databases. | L. Submitted (AdC-2001) to the EMBL/GenBank/DbBJ databases. | PEMBL; AF291822; AAG01549.3; | THE ABC TRANSPORTER FAMILY. | EMBL; AF291822; AAG01549.3; AA. | InterPro; IPRO01366; AA.TRNA.ligase_II. | InterPro; IPRO01406; AA.C.transporter_tmem. | InterPro; IPRO01409; ABC_transporter. | InterPro; IPRO01439; ABC_transporter. | InterPro; IPRO0164; ARC_membrane; 2. | Pefam: PF00005; ABC_trans; 2. | Pefam: PF00005; ABC_transporter. | Pefam: PF0
                                                                                                                                                   ALDTQSERLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLR 1248
                                                                                                                                                                                          QGRLPARPMLWILSSLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATS 1188
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                                           FLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 ------YLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSF
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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1331 AA; 145283 MW; E35B7AFCE3043E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%; Score 1971.5; DB 3; 36.6%; Pred. No. 4.7e-125; ive 208; Mismatches 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport.
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01-0CT-2001 (TrEMBLRE). 18, Last

01-DEC-2001 (TrEMBLRE). 19, Last

MULTIDRUG RESISTANCE PROTEIN MDR.
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                                                                                                                                                                                                                                                                                                           1249 GRYYEMCLAQSL 1260
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NCBI_TaxID≈5551;
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985 SVAKSSILYAASQSFSFFCLALGF-----WYGGGLLGKGEYNAFQFFLCISCVIF--GS 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEM 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPRLYRGHMSLVQQEPTLYQGSVRENVTLALEA-ELSEELCQGRLPARPMLWILSSLYQK 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1148 ALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEAST 1207
                                           313 GKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGC 372
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                                                                                                                                                                                      GRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREKQM-EL 491
                                                                                                                                                                                                                                                                                             ALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISOGKIVEOGTHHELIEFG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 STTLI-----VALTVALAFGW-------KLALVCISTVPVLLLCGFYRFW 928
                                                                                                                                                 GTYLOLVEAQKINEERGEESEDEAVLEKEKEISRQISVPAKSVNSGKYPDEDVBANLGRI
                                                                                                                                                                                                                                                                                                                                                                                                      HTTATSQAGDLEKRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLSTITVLICAATFPGQ
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241 YWKLALICSSTIVAMILVMG-GISRFVVKSGRMTLVSYGEGGTVAEEVISSIRNATAFGT
                         253 QKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADV
                                                                                                                                                                                                                                          492 VOKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATS
                                                                                                                                                                                                                                                                                                                                                    612 CHYAALVRAQDLGAD--EQOEHEKTLHEK------AAREAAGERP-----ALERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLFSRLLTVFELSGH----AAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       839 ARSKSFRAMLRODIAFFDLPENSTGALTSFLSTETKHLSGVSGATLGTILMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTSLWMETGPGGCVWCTSTPAFGWLPQNSSRDEARSRKLGKLC-------RKCW
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                                                                                                                                    LGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879 ACKRSSYRDPDRLIFDSRRPCSPTVLGHV-----EQGLAKIIQSFWFGR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 DPDRQSGTKAYFRVWGYSSVQDHVIRVTGLFAAIACGAALPMMTLVFGTLIDNFNDWGAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 DGSPEAFKADVDHFVLWFVYLFIGKFVLTYVSTAAITISAIRTTRTLRRVFLECTLRQEV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 VIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angermayr K., Parson W., Stoffler G., Haas H.; "Expression of atrC-encoding a novel member of the ATP binding cassette transporter family in Aspergillus nidulans-is sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 WHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 LOQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
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                                                                                                                                                                                                                                                     Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ABC TRANSPORTER PROTEIN ATRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%; Score 1968.5; DB 3;
llarity 36.1%; Pred. No. 7.3e-125;
Conservative 243; Mismatches 487;
                                                                                                                                                                                Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungl; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=5072;
PRT: 1293 AA.
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MEDLINE-99156773; Pubmed-10036328;
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Best Local Similarity
Matches 466; Conserv
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PROSITE; PS00211
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01-JON-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MULIIDRUG RESISTANCE PROTEIN 1.
MDR1.
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                                                      ----DLGADE--QQEHEKTLHEKAAREAAGERPALERTHTTATSQAGDLEKRKVPVGTL
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                               503 VFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQ
                                                                                                      563 EALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQ-
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SEQUENCE FROM N.A.
STRAIN=10AF/86/10;
MEDLINE=98038972; PubMed=9373135;
Tobin M.B., Peery R.B., Skatrud P.L.;
"Genes encoding multiple drug resistance-like proteins in Aspergillus funigatus and Aspergillus flavus.";
dene 200:11-23(1997).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL; U62933; ABB88558.1;
HSSP; P13569; NUBD.
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SEOUENCE 1349 Aa; 147723 MW; B90A86F9D62C4165 CRC64;
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                                                                                                                                                                                                                                                                                         Interpro; IPR003593; AAA.
Interpro; IPR00140; ABC_transporter_tmem.
Interpro; IPR003499; ABC_transportr.
Interpro; IPR001687; APP GTP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
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PROSITE; PS00211; ABC_TRANSPORTER; 2.
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                                                                                                                                                                                                                                                                                TKARSAANYILWLRTLKPTIR-ETEENKKKGPVGGCPVDLEDIEFRYRQRDSARVLRGVS 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       043140;

01-304-1998 (TrEMBLrel. 06, Created)

01-JUN-1998 (TrEMBLrel. 19, Last annotation update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

MULTIDRUG RESISTANCE PROTEIN 1.

MULTIDRUG RESISTANCE PROTEIN 1.

Cryptococcus neoformans (Filobasidiella neoformans).

Cryptococcus neoformans (Filobasidiella neoformans).

Pumellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

NCBI_TaxID-5207;
                                                                                                         DIELLDIPEQISGALTSQLSALPTQLQEL------ISANFLIYIVVGQHRLE 828
                                                                                                                                                                       VCISVVPILLACG-----FLRFYMLAQFQQRSKSAYEGSASYACEATSAIRTVASL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEATAIN-M.1106;
MEDLINE-98072425; PubMed-9409767;
Thornewell S.1. Peery R.B., Skatrud P.L.;
Thornewell S.2. Peery R.B., Skatrud P.L.;
Cloning and characterization of CnewDR1: a Cryptococcus neoformans
gene encoding a protein related to multidrug resistance proteins.";
Gene 201:21-29(1997).
EMBL: U62930; AAC49890.1: --
EMBL: U62930; AAC49889.1: --
EMBL: U62930; AAC49889.1: --
                     RKVPVGTLGYSLLKCI-LIMFYEOKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFE
                                     KKVPEQFEKYSLWTLVKFIGAFNRPELGYMLIGLTFSFL-AGGGQPTQAFLYAKAISTLS
EAEALEADADMDADDFGQEGVTRIKTAVSSSNSLDAVDEKARLEMKRTGTQKSVSSAVLS
                                                                LSG---HAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQ
                                                                                      LPESMFHKLRHDANFWSLMFFVVGIAQFISLSINGTAFAICSERLIRRARSQAFRSILRQ
                                                                                                                       CRK -- CWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQS
                                                                                                                                                                                                                                     932 MEFLAIALGFCIAVDNWLQVSTTQLN-----FISSSWAFCLPVQAAAQYLAYSTSF
                                                                                                                                                   QC-STTSLWMETGPGGCVWCTSTPAFGWLPQNSSRD-------EARS--RKLGKL
                                                                                                                                                                                                                                                                                                                                                                                                             1151 RLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTSRT
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InterPro; IPR002106; AA_tRNA_ligase_II
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389 EQSKIVGRKGSIFEGFGLSIMFFVIYAAYALAPFYGGILVSNGQ-ADSGIVINVFMSILI 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 AATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 YNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQ-RDLPREKQMELVQKACKASNGDV 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 -NLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQ 807
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNY -----NSGDGSPEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 IPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 APLEIIAMVLGLVLAVAAGSCOPLMTLIFGRLTTSFTNYAVIANOISOGGLTPETSAALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FRADVDHFVLWFVYLFIGKFVLTYVSTAAITISAIRTRTLRRVFLECTLRGEVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 OQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                564 ALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELI--EFGCHYAALVRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             700 TITVLICAATFPGQALLFSRLLTVFELSG-----HAAQERADFYILMFFVVALG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 FINELPNGYETEVGERAGALSGGGRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQE
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                                                                                                                                                                                                                                                                                                                                            Query Match 27.7%; Score 1789.5; DB 3; Length 1408; Best Lecal Similarity 34.4%; Pred. No. 1.2e-112; Matches 478; Conservative 214; Mismetches 493; Indels 203;
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR001439; ABC_transportr.
InterPro; IPR001643; ATP_GTP_A,
Pfam; PF00064; ABC_tran; 2.
Pfam; PF00005; ABC_tran; 2.
PRART; SM00182; AAA,
PROSITE; PS00139; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport
SEQUENCE 1408 AA; I52143 MW; CEBA34A09A6F69F8 CRC64;
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                                                                                                                                                                                                                                                                                                                            1136 -PMLWILSSLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQS 1194
                                                                                                   996 GGYIRLKVVVLKDQRMKKLHAASAHLASEAAGAVKTVASLTREK-----DVRRIYSEALK 1050
                                                                                                                                          SWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIR-ETEENK---KKGPVGCC 1017
                                                                                                                                                                                                                    PVDLEDIEFRYRQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGR 1077
                                                                                                                                                                                                                                                                                                                                                           ERLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEM 1254
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SEQUENCE FROM N.A.
SEQUENCE 70 N.A.
MEDLINE-98038972; PubMed-9373135;
MEDLINE-98038972; PubMed-9373135;
Toblin M.B., Peerry R.B., Skattud P.L.;
Toblin M.B., Peerry R.B., Skattud P.L.;
Toblin M.B., Peerry R.B., Skattud P.L.;
Genes encoding multiple drug resistance-like proteins in Aspergillus fumigatus and Aspergillus flavus.";
Gene 200:11-23(1997).
EMBL: U62932; AAB88656.1;
EMBL: U62932; AAB88655.1;
EMBL: U62931; ABB88655.1;
VOGLEGPILGTVV-----OSCATLI-----GGCIIGLCYGPLLALIGIACIPILVS 995
                                                                             -GWL------PQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVL 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus flavus.
Eukaryota: Fungi: Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID-5059;
                                                                                                                         GHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWL---QVSTTQLNFISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01.JUN-1998 (TIEMBLIE). 06, Greated)
01.JUN-1998 (TIEMBLIE). 06, Last sequence update)
01.JUN-1998 (TIEMBLIE). 19, Last annotation update)
01.DEC-2001 (TIEMBLIE). 19, Last annotation update)
                                LOELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGC-----
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Interpro: IPR0013693; AAA.
Interpro: IPR00140, ABC_transporter_tmem.
Interpro: IPR001687; ATP_GTP_A.
Interpro: IPR001687; ATP_GTP_A.
Ffam: PR00664; ABC_membrane; 2.
Ffam: PR00005; ABC_tran; 2.
SMART; SMORTS; SMORTER; 2.
ATP-binding; Transport.
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                                                                                                                                                                                                                                                                                  VQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVL 236
                                                                                                                                                                                                                                                                                                                                                    296
                                                                                                                                                                                                                                                                                                                                                                                                                     FWMGSRFLVEG-ISNIKAGDVLTIMMAIILGSYNLGNVAPNGQALSDAVAAASKLYGTID 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYEQKNLY------WCFLLSTITVLICAATF-PGQALLFSRLLTVFE---LSGHAA 731
                                                                                                                                                                                       IGSGASLPLMSIIFGSFTNKFNNYNSGDGSPEAFKADVDHFVLWFVYLFIGKFVLTYVST 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWKGFRMYQNGEVADV--GKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIID 354
                                                                                     Gaps
                                                                                                                                           7 RPRPNQDGSESS----SHPPP----EKETEGSISDYLRIFRYADKYDWTLNVIALICA 56
                                                                                                                                                                                                                                                                                                                                                                                                AEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 VISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHEKTLHEKAAREAAGERPALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605 VLANGQIVEQGPHEHIMDRRGIYCDMVEAHEI------KKRYSRYSKRYSQLLTNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 QERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASG
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                                                                                                                                                                                                              Indels 172;
                                                Length 1307;
2F65C12CF27FE5F3 CRC64;
                                                Ouery Match 27.6%; Score 1780; DB 3; 18est Local Similarity 34.3%; Pred. No. 4.8e-112; Matches 466; Conservative 222; Mismatches 500;
143874 MW;
 1307 AA;
 SEQUENCE
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                                                                                                                 1044 IEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQE 1103
                                                                                                                                                                                                                                                                                     GGORORIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTSRTTIAVAHRLSTI 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Archosaurla; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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   -- YASSQALPFFC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMIFGSLLAIAHGTSLPIAMIIFGDMTDSFVTSGMTNITGNSSGLNSSADVFNKLEBEMT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYAYYYSAIAAAVLVAAYIQTSFWTLAAGRQVKKIREKFFHAIMRQEIGWFDVNDAGELN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 TXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGIC 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADESEKPRPNODG-----SESSSHPPPEKETEG-----SISDYLRIFRYADKYDWT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-INTESTINE:
MEDLINE-99209805; PubMed-10195430;
Edelmann H.M.L., Duchek P., Rosenthal F.E., Foeger N., Glackin C.,
Edelmann H.M.L., Duchek P., Rosenthal F.E., Foeger N., Glackin C.,
"Cardell, a chicken P-glycoprotein, confers multidrug resistance and
interacts with Estradiol.";
EMBL: Annoy99; CAA08835.1;
HNSP: P13569; LNED.
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                              937 IALGFCIAVDNWL------QVSTTQLNFISSSWAFCLPVQAAAQYLAYSTSFTKARSA
                                                                                            ANY ILWLRTLKPTIRE--TEENKKKG-PVGGCP--VDLEDIEFRYRORDSARVLRGVSMT
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1288 AA; 141917 MW; CB258A5F2826DB6C CRC64;
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Last annotation update)
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932 TVVSLTMETEALQSYQAQLRRQLKSDILPIVKSSLL---
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1213 ALDTESEKIVQEALDKAREGRTCIVIAHRLSTIQNADKIAVIQNGKVIEQGTHQQLLAEK 1272
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Eukaryota, Metazoa; Chorada; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
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MEDLINE-9332ASI; PubMed-7599185;
A CASILING G., Shen H.J., Horwitz S.B.;
Castillo G., Shen H.J., Horman S.B.;
Castillo 
                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOC-2001 (TrEMBLrel. 19, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN.
                                                                                                                                                                                      PRT; 1287 AA
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
NCBL_TaxID=8355;
                                      1249 GRYYEMCLADS 1259
                                                                           1273 GEYYSLVNVQS 1283
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SEQUENCE FROM N.A.
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1088 MSPRLYRGHMSLVQQEPTLYQGSVRENVTLALEAEL--SEELCQGRLPARPMLWILSSLY 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                           920 FGRCFG--FHLSQSMEFLAIA----LGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQAAA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      668 STRRSIHAPQGODRK--LGTKEDLNENVPSVSFWRILKLNSTEWPYPVVGIFCAIINGGL 725
                                                                                                                          710 FPGQALLFSRLLTVF--ELSGHAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVV 767
                                                                                                                                                                                                                                                     768 THRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQLQELISANFLIYIVVGQHRL 827
                                                                                                                                                                                                                                                                                                                                                                            865 ARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQ----SFW 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889 KELEGAGKIATEA------IENFRTVVSLTREQKFEYMYAOSLQVPYRNSLR 934
   HTTATSQAGDLEKRKVPVGT---LGYSLLKCILIMFYEQKNLYW-CFLLSTITVLICAAT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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-1 - SIMILARIYY: BELOGS TO THE ABC TRANSPORTER FAMILY.
EMBL: 078609; AAB58489.1; ...
INTERPLO; IPR0013593; AAA.
INTERPLO; IPR0013593; AAA.
INTERPLO; IPR001140; ABC_Lransporter_tmem.
InterPro; IPR001687; APC_CTRANSPORTE.
InterPro; IPR001687; APC_GTP_A.
PEAM: PF00664; ABC_Incenbrane; 2.
PEAM: PF00605; ABC_Lran; 2.
SWART; SM00382; AAA; 2.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN-1.
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Longley M., Crawford A.M.;
"Ovine mdri gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 TRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID-9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELiefgchyaalvraodlgadeqoehektlhekaareaagerpale------rt
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                                                                                                                                                                                                                                                                    Puel O., Lepage J.F., Alvinerie M., Galtier P., Pineau T., Submitted (JAK-1989) to the EMBL/GenBank/DDBJ databases.

-1 SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

EMBL: AF045016; AAC02113.1; -1

INTERFO: IPR003593; AAA.

INTERPO: IPR00140; ABC_transporter_tmem.

INTERPO: IPR00140; ABC_transporter_tmem.

INTERPO: IPR001687; ATP_GTP_A.

Pfam: PF00664; ARC_membrane. 2.

Pfam: PF00605; ARC_transports.

Pfam: PF00605; ARC_transports.

PMARP: SW00302; AAA, 2.

PROSITE: PS00211; AAA, 2.
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MULTIDRUG RESISTANCE P-GLYCOPROTEIN
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                                                                                                                                                                                  72 SFTNKF-------NNYNSGDGSPEAFKADVDHFVLWFVYLFIGKFVL--TYVS 115
                                                                                                                                                                                                   116 TAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVF 175
                                                                                                                                                                                                                                                         176 TVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAV 235
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                                                                                                                                                                                                                                                                                                                                                                    296 AFWRGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDK 355
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AFWYGTSLVLSREYS-IGQVLTVFFSVLIGAFSIGQASPNIEAFANARGAAYEVFKIIDN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGS 415
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                                                                                               Gaps
                                                                                                                                           12 ODGSESSSHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFG 71
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                                                                                               Indels 112;
                                                                     Length 1285;
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Transport.
SEQUENCE 1285 AA; 142020 MW; 90153E617C44856F CRC64;
                                                                   25.4%; Score 1640; DB 6; larity 32.4%; Pred. No. 1.5e-102; Conservative 247; Mismatches 527;
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                                                                               Best Local Similarity
Matches 425; Conserv
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                                                    936 SLRRAHVFGITFSITQAMMYFSYAGCFRFGAYLVAQGIMEFQDVLLVFS----AVVFGAM 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 1A.
Rattus norvegicus (Rat).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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RA Meijer D.K.F., Muller M.;

RA Meijer D.K.F., Muller M.;

RA Meijer D.K.F., Muller M.;

R. Cloning and functional characterization of the rat multidrug resistance protein Muller M.;

R. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

R. Submitted (APR-2000) to THE ABC TRANSPORTER FAMILY.

DR InterPro; IPR001359; AAA.

DR InterPro; IPR00139; ABC_transportr.

DR InterPro; IPR001687; ARC_transportr.

DR InterPro; IPR001687; ARC_transportr.

DR InterPro; ABC_mansportr.

DR Pfam; PF00664; ABC_mansportr.

DR Pfam; PF00664; ABC_mansportr.

DR Pfam; PF00111; ABC_mansportr.

DR Pfam; PF00111; ARA.

DR Pfam; PF00111; ABC_mansportr.

DR Pfam; PF00111; ABC_mansportr.

DR SMART; SM03121; AAA; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
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SFWFGRCFG--FHLSQSMEFLAIA----LGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQ
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GAVAEEVLAAIRTVIAFGGQKKELERYNNNLEEAKRLGIKKAITANISMGAAFLLIYASY
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LQGFTFGKAGEILTKRLRYMVFKSMLRQDISWFDDPKNTTGALTTRLANDAAQVKGATGS
                                                    AVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAI
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                                    174 VFTVQALSMFFSAFVVALASQWKLALITMSVIPAJFLVTGICIAIDAAQEARITRIYSRA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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243 GAVAEEVLAAIRTVIAFGGQKKELERYNNNLEEAKRLGIKKAITANISMGAAFLLIYASY
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                                                            RTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELORLRGRYYEMCLAQS 1259
                                                                                             1023.1; -. 140343 MW; D9A17457362DA0ED CRC64;
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY:
Yamazaki M., Leake B.F., Kim R.B.;
Yamazaki M., Leake B.F., Kim R.B.;
"Molecular Cloning of Rat Mdria cDNA.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF2686167; AAR33023.1;
SEQUENCE 1272 AA; 140343 MW; D9A17457362DA0ED CRC64;
                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P-GLYCOROTEIN.
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Conservative 252; Mismatches
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MEDLINE-94150716; PubMed-7906398;
MEDLINE-94150716; PubMed-7906398;
Wilson R., Anscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Anscough R., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
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Bukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCRI_TaxID=6239;
                                                      876 LKDKKELEGSGKIATEA-----IENFRIVVSLIREQKFETMYAQGLQIPYR
                                                                                                                                                                                                                                             593 ISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHE----KTLHEKAAREAAGERP
                   593 FDGGVIXEQGNHDELMREKGIYFKLVMAQTAGNEIELGNEACESKDGIDNVDMSSKDSGS
                                                                               LLSTITVLICAATFPGQALLFSRLUTVFELSG--HAAQERADFYILMFFVVALGNLVGYF
                                                                                          --ALPTOLOELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNS
                                                                                                                                                                          824 RLAVITONIANLGTGIIISLIYG------WQLTLLLLAIVP--IIAIAGVVEMKMLSGQA
                                                                                                                                                                                             SRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVE----QGLA----
                                                                                                                                                                                                                                 913 -KIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQA
                                                                                                                                                                                                                                                                      972 AAQYLAYSTSFTKARSAANYILWLRTLKPTIRE-TEENKKKGPVGGCPVDLEDIEFRYRQ
                                                                                                                                                                                                                                                                                                           RDSARVLRGVSMTIEPGGFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSP
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                                                                                                                                                                                                                                                                                                                                                                                   1149 LKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTS
                                            ALERTHTTATS-----QAGDLEKRK-----VPVGTLGYSLLKCILIMFYEQKNLYW-CF
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01-NOV-1998 (TFEMBLZEL. 0
01-DEC-2001 (TFEMBLZEL. 1
C47A10.1 PROTEIN.
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Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Eatreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Barsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Markson A., Weinstock L., Wilkinson-Sproat J., Wohldman P., R., 2 Mb. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 AGFLQASCFMVICEKLSNRFRRQFFHSVMRQEIAWYDKNTSGTLSNKLFDNLERVREGTG
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                                                                                                                                                                                                                                                                                                                                                             Basham V.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
EMBL, 293782; CABO7855.1; -
EMBL, 281484; CABO7855.1; -
EMBL, 281484; CABO3973.1; -
EMBL, 293782; CABO3973.1; JOINED.
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PROSITE; PSOU42; ZINC_PROFEASE; UNKNOWN_1.
ATP-binding; Transport,
SEQUENCE 1294 AA: 142490 MW; DDBED2602F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003593, AAA.
InterPro; IPR00140; ABC_transporter_tmem.
InterPro; IPR00140; ABC_transporter_tmem.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR001087; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00665; ABC_tran; 2.
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        104 IYIFFAIIAALIQGAVMPAFSLFFSQIINVFSNPDRDQMKKDGH-----FWALMFLVL 756
                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
P-GINCOPROTEIN-LIKE PROETIN.
17J13.110.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                      695 CFL-LSTITVLICAATFPGQALLFSRLLTVF-----ELSGHAAQERADFYILMFFVV 745
                                                                                                                                                              ALGNLVGYFTIGWTCN---VISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQL- 801
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                                                                                           RIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGN
                                      590 IAVISQCKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHENTLHEKAAREAA----
                                                  ------GERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCILIMFYEQKNLYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00664; ABC_tran; 2.
SNART; SN00382; AAA, ABC_TRANSPORTER; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROSITE; PS00095; CS_MTASE_2; UNKNOWN_1.
ATP-binding; Transport.
SEQUENCE 1292 AA: 139754 MW; 9C95DF3AC84E7432 CRC64;
      Мемев
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Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.,
Submitted (FEB-2000) to the EMBL/Genamk/DobiJ databases
                                                                                                                                                                                                    SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

EU Arabidopsis sequencing project;

SUDMITTED (FEB-2000) to the EMBL/GenBank/DDBJ database:

SUDMITTED (FEB-2000) to the EMBL/GenBank/DDBJ database:

SMELIA AL188651;

INTERPRO | IPR001353;

AAA.

INTERPRO | IPR00140;

INTERPRO | IPR00140;

INTERPRO | IPR00140;

INTERPRO | IPR001687;

INTERPRO | IPR001687;

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972 AGARLVDDG---KTTFDSVFRVFFALJMAAVAISQSSSLSPDSSKASNAAASIFAVIDRE 1028
                                                                                                                                                                                                                                                                                                                              1000 PTIRETEENKK-----KGPVGGCPVDLEDIEFRYRQRDSARVLRGVSMTIEPGGFVAYVG 1054
                                                                                                                                                                                                                                                                                                                                                 1055 ASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVREN 1114
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                                                                                                                                             927 -----GFGVSFFVLFSSFAASFY 971
                                                                                                                                                                                                                                                                               943 IA----VINWLQVSTTQLNFISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLK 999
                                                                                        883 SSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLAIALGFC 942
646 QTEDSTDEQKLSME----SMKRSSLRKSSLSRSLSKRSSSFSMFGFPAGIDTNNEAIP 699
                         677 ----SLLKCILIMFYE----QKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFE 725
                                               700 EKDIKVSTPIKEKKVSFRVAALNKPEIPMLILGSIAAVLNGVILPIFGILISSVIKAFF 759
                                                                         726 LSGHAAQERADFYILMFFVVALGNLVG-----YFTIGWTCNVISQVVTHRYQAAMFQRV 779
                                                                                                                          780 LDQDIELLDIPEQISGALTSQLS------ALPTQLQELISANF-LIYIVVGQHR 826
                                                                                                                                                                            827 LEQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNSSR---DEARS-RKLGKLCRKCWACKR 882
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Search completed: April 27, 2002, 07:58:10 Job time: 726 sec

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burpean Bioinformatics institute. There are no restrictions on its use by non-profit institutions in the area no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    streptococc
rattus norv
candida alb
haemophilus
                                                                                                                                                          mus musculu
cricetus cr
mycobacteri
                                                                                                                            leishmania
homo sapien
                    rattus norv
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-- FUNCITION: MAY BE A TRANSMERRANE TRANSFORTER OF THE MATING
FACTOR, NAMELY P-FACTOR OR M-FACTOR. CONFERS RESISTANCE TO
LEPTOMYCIN B AND TO SEVERAL OTHER ANTIFUNGAL DRUGS.
-- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
--- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Antibiotic resistance. CYTOPLASMIC (POTENTIAL). POTENTIAL. POTENTIAL.
P21958 n
P36372 n
O15440 b
P53598 c
P63706 p
P21441 p
P21441 p
P33527 p
P33527 c
O09427 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                         PMD1_SCHPO STANDARD; PRT; 1362 AA. PPG1515, O74513; O1-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Lepcomycin B resistance protein pmd1.
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Interpro; IPR001140; ABC_transporter_tmem.
Interpro; IPR001140; ABC_transporter_tmem.
Interpro; IPR001487; ABC_transportr.
PEAM; PF00664; ABC_membrane; 2.
PEAM; PF000664; ABC_membrane; 2.
PROSITE; PS00121; ABC_TRANSPORTER; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROMAIN.
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10 91 115 POTENTIAL.
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                                                                                                                                                                                                                                                       ALIGNMENTS
                                                    EXP8_STRPN
ACC8_RAT
HST6_CANAL
MSBA_HAEIN
MDR_LEITA
MRP1_HUMAN
                                                                                                                                                            TAP2_MOUSE
ACC8_CRICR
YC72_MYCTU
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  724
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PMD1_SCHPO
    (without alignments)
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mus musculu
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mus musculu
homo sapien
caenorhabdi
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plasmodium
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P08183 homo sapien
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                                                                                                                          April 27, 2002, 07:59:41; Search time 35.22 Seconds
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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MDR3_CRIGR
MDR1_RAT
MDR1_CAEEL
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MRP6_HUMAN
TAP1_RAT
MRP5_MOUSE
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MDR1_MOUSE
MDR3_MOUSE
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MAM1_SCHPO
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YFX9_SCHPO
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Gapop 10.0 , Gapext 0.5
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Chen C.-J., Chin J.E., Ueda K., Clark D.P., Pastan I., Gottesman M.M.,
Roninson I.B.;
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CAATFPGQALLFSRLLTVF-ELSCHAAQERADFYILMFFVVALGNLVGYFTIGWTCNVIS 764
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Cell 47:381-389(1986).

SEQUENCE FROM N.A.

MEDLINE-90094448; PubMed=1967175;

Chen C.-J., Clark D.P., Ueda K., Pastan I., Gottesman M.M.,

Ronlinson I.B.;

Genomic organization of the human multidrug resistance (MDR1) gene
and origin of P-glycoptoclais.

J. Biol. Chem. 265:506-514(1990).
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P08183: 012755; Q14812;

P08183: 012755; Q14812;

P01-402-1988 (Rel. 08, Created)

O1-407-1997 (Rel. 35, Last sequence update)

16-027-2001 (Rel. 40, Last annotation update)

MULIGARY FESISEANCE Protein 1 (P-91ycoprotein 1).

ABCB1 OR PGY1 OR MRH.

BUNARYOCIA METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.

DISTRIBLY STRONG S. Steper K.A. Lacayo N.J., Jaffrezou J.P.,
Chen G., Duran G.E., Steper K.A. Lacayo N.J., Jaffrezou J.P.,
Dumontet C., Sikic B.I.;
Multidrupt-resistant human sarcoma cells with a mutant P-glycoprotein,
altered phenotype, and resistance to cyclosporins.";
J. Biol. Chem. 272:5974-5982(1997).
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SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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Dubnitded (JUL-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ENERGY-DEFENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
BRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, SMALL INTESTINE
                                                                                                                                                                                                                           SEQUENCE OF 178-215 AND 600-856 FROM N.A.
MEDLINE-90290529; Pubmed-1972623;
Gekeler V., Weger S., Probst H.;
"mdri/P-91ycoprotein gene segments analyzed from various human leukemic cell lines exhibiting different multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-23 FROM N.A.
Kioka N., Tsubota J., Kakehi Y., Komano T., Gottesman M.M.,
                                                                                                                                                                       Smith A., Beck C., Gibson A.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            profiles.";
Biochem. Biophys. Res. Commun. 169:796-802(1990).
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EMBL, M29447, AAA59576.1;
EMBL, M29421, AAA59576.1;
EMBL, M29426, AAA59576.1;
EMBL, M29426, AAA59576.1;
UN29427, AAA59576.1;
UN29427, AAA59576.1;
UN29428, AAA59576.1;
UN29429, AAA59576.1;
UNED, EMBL, M29431, AAA59576.1;
UNED, EMBL, M29431, AAA59576.1;
UNED, EMBL, M29431, AAA59576.1;
UNUED, EMBL, M29431, AAA59576.1;
UNUED, EMBL, M29431, AAA59576.1;
UN29431, AAA59576.1;
UNUED, EMBL, M29438, AAA59576.1;
UNUED, EMBL, M29438, AAA59576.1;
UNUED, EMBL, M29439, AAA59576.1;
UNUED, EMBL, M29441, AAA59576.1;
UNUED, EMBL, M29441, AAA59576.1;
UNUED, EMBL, M29441;
AAA59576.1;
UNUED, EMBL, M29444;
AAA59576.1;
UNUED, MAS9676.1;
UNUED, MAS9676.1;
UNUED, MAS9676.1;
UNUED, MSS676.1;
UNUED, MSS
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PIR; A34914; A34914.
MIM; 171050; -
InterPro; IPR003593; AAA.
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LPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREK- 487
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InterPro; IPR001439; ABC_transportr.
InterPro; IPR001687; APC_TROP_A.
Pfam; PF000664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
Pfam; PF00005; ABC_tran; 2.
PRART: SM00182: AAA_2.
PROSTIE; PS00211; ABC_TRANSPORTER; 2.
ATP_binding; Glycoprotein; Transmembrane; Transport; Repeat;
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445 DPTEGMVSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYG------RENV 495
                                   QMELVQKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLD 547
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                                                        EATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHEL
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01-MAY-1991 (Rel. 18, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
ABCB4 OR PGY3 OR MDR3.
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- SUBCELLULAR LOCATION: Integral membrane protein.

- DISBASE: DEFECTS IN ABEGA ARE A CAUSE OF PROCRESSIVE FAMILIAL.

- DISBASE: DEFECTS IN ABEGA ARE A CAUSE OF PROCRESSIVE FAMILIAL.

- INTRAHEPATIC CHOLESTASIS TYPE III (PPIC), A FORM OF AUTOSOMAL.

RECESSIVE LIVER DISGRESSES, CHARACTERIZED BY EARLY ONSET OF CHOLESTASIS THAT PROGRESSES TO CIRRHOSIS AND LIVER FAILURE BEFORE ADULTHOOD.

- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3101. Chem. 266:5303-5310(1991).
FUNCTION: ENERGY-DEPENDENT EFPLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS. HUMAN MDR3 IS NOT CAPABLE OF COMFERRING DRUG SESISTANCE. MEDIATES THE TRANSLOCATION OF PHOSPHATIDYLCHOLINE ACROSS THE CANALLCCULAR MEMBRANE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
MEDELNE STRUCTURE,
MEDINE-91161629; PubMed-2002063;
Lincke C.R., Smit J.J.M., van der Velde-Koerts T., Borst P.;
Lincke C.R., Smit J.J.M., van der Velde-Koerts T., Borst P.;
"Structure of the human MDR3 gene and physical mapping of the human MDR Locus.";
J. Biol. Chem. 266:5303-5310(1991).
-I- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED
                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 856-1279 FROM N.A.
MEDLINE-88111519; PubMed-282568;
Wan der Bliek A.M., Baas F., ten Houte de Lange T., Koolman P.M.,
van der Welde-Koerts T., Borst P.,
"The human mdi3 gene encodes a novel P-glycoprotein homologue and
gives rise to alternatively spliced mRNAs in liver.";
EMBO J. 6:3325-3331(1987).
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-69138016; Pubmed-2906314;
van der Bliek A.M., Koolman P.M., Schneider C., Borst P.;
"Sequence of mar3 cDNA encoding a human P-glycoprotein.";
Gene 71:401-411(1988).
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InterPro; IRR001140; ABC_transporter_tmem.
InterPro; IRR001140; ABC_transporter_tmem.
InterPro; IRR001687; ARC_transportr.
Pfan; PP00664; ABC_membrane; 2.
Pfan; PP00065; ABC_tran; 2.
PKART; SM00382; AAA; 2.
PKOSITE; PS00211; ABC_TRANSPORTER; 2.
ARP-binding; Glycoprotein; Transmembrane; Tra
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EMBL: X06181; CAA29547.1; -...
PIR: JS0051; DVHU3.
PIR: A42213. A42213.
HSSP: P13569; INBD.
                                Mammalia; Eutheria;
NCBI_TaxID=9606;
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W, 3D58C98B5C8D6087 CRC64;
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                                                                       CYTOPLASMIC (POTENTIAL).
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ATP (BY SIMILARITY).
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MEDLINE-9104253; PubMed-2248681;
Raymond M., Gros P.; PubMed-2248681;
Raymond M., Gros P.; PubMed-2248681;
Raymond M., Gros P.; PubMed-2248681;
Cell. Specific activity of cis-acting regulatory elements in the mouse multidrug resistance gene mdrl.";
Mol. Cell. Biol. 10:6034-6040(1990).
-1. FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASE DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-1. SUBCELLULAR LOCATION: Integral membrane protein.
-1. PTM: SEVERAL PHOSPHORYLATED SERINE RESIDUES ARE PRESENT IN THE
                                                               896 RRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQ
                                                                                               918 M------YVEKLYGPYRNSVOKAHIYGITFSISOAFMYFSYAGCFRFGAYLIVN-GH
                                                                                                                                 956 LNFISSSWAFCLPVQAAAQYLAYSTSF----TKARSAANYILWLRTLKPTIRE-TEENKK
                                                                                                                                                      1071 YDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLALEAEL--SEELC
                                                                                                                                                                                                                                                                                                                                       129 OGRLPA--RPMLWILSSLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEA
                                                                                                                                                                                                                                                                                                                                                          836 WMETGPGGCVWCTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDS
                            860 LLAVVP--IIAVSGIVEMKLLAGNAKRDKKELEAAGKIATEAIENIRTVVSLTQERKFES
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Raymond M., Gros P.;
"Manmalian mulidfury;
"resistance gene: correlation of organization with structural domains and duplication
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01-JAN-1988 (Rel. 05, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Multidrug resistance protein I (P-glycoprotein 1).
ABCBI OR PGYI OR PGYI-I OR MDRI OR MDRIB.
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                 IN MOUSE THE MDR GENE FAMILY INCLUDES THREE OR MORE
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                                RELATED BUT DISTINCT CELLULAR GENES.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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M-LINKED (GLCNAC. .) (POTENTIAL).
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InterPro: IPR001140; AAD.
InterPro: IPR0013593; AAD.
InterPro: IPR003439; AAC.transporter_tmem.
InterPro: IPR001687; ATP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
SMART; SM00182; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
APP-binding; Glycoprotein; Transmembrane; Transport; Repeat; Multigene family; Phosphorylation.
DOMAIN.
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EEMBL; M60348; AAA3513.1; -.
PIR; A33719; DVMS1.
MGD; MGI:97568; Abcbl.
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N-LINKED (GLCNAC. .) (POTENTIAL).
QL -> HV (IN REF. 2 AND 3).
F -> S (IN REF. 2 AND 3).
F -> V (IN REF. 2 AND 3).
F -> V (IN REF. 2 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 GASGSGKSTMYGLLERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 GNSGCGKSTTVQLMQRLYDPLDGMVSIDGQDIRTINVRYLREIIGVVSQEPVLRATTIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 NIANGFMDEQRDLPREKQMELVQKACKASNGDVFINELPNGYETEVGERAGALSGGQRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1627.5; DB 1; Length 1276; Pred. No. 1.2e-97; Mismatches 559; Indels 81;
                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                            POTENTIAL. POTENTIAL.
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90 90 N-LIN
526 527 QC ->
939 939 F ->
1036 1036 F ->
1276 AA; 140754 MW; 7
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984
1276
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Best Local S
Matches 419,
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alreament (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A, MEDLINE-90205845; PubMed-1969610; Devault A., Gros P.; "Two members of the mouse mdr gene family confer multidrug resistance with overlapping but distinct drug specificities."; Mol. Cell. Biol. 10:1652-1663(1990).
                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural analysis of the mouse mdrla (P-glycoprotein) promoter reveals the basis for differential transcript heterogeneity in multidrug-resistant J774.2 cells "; Mol. Cell. Biol. 10:3596-3606(1990).
                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
MEDLINE-90287150; PubMed-1972547;
HSU S.I.H., Cohen D., Kirschner L.S., Lothstein L., Hartstein M.,
HOTWitz S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL; M30697; AAA39517.1; ...
R EMEL; M3581; AAA39517.1; ...
R EMBL; M3581; AAA39514.1; ...
R EMBL; M34785; DAA39518.1; ...
R PIR; A34175; DVMS1A.
R PIR; A34175; DVMS1A.
R DIR; A34786; MGI: 97570; Abch4.
R InterPro; IPR0013593; AAA.
R InterPro; IPR0013693; AAA.
R InterPro; IPR00140; ABC_transporter_tmem.
R InterPro; IPR001687; ATP_GTP_A.
R Pfam; PF00005; ABC_transporter_
R Pfam; PF00005; ABC_transporter_
R Pfam; PF00005; ABC_transporter_
R PR0511E; PS00011; ABC_TRANSPORTER; 2.
R PRO511E; PS00011; ABC_TRANSPORTER; 2.
M ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat; Multigene family.
                                                                                                     01-AMY-1991 (Rel. 18, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Multidrug resistance protein 3 (P-glycoprotein 3) (MDRIA).
ABCB4 OR PGY3 OR PCY-3 OR MDR3 OR MDRIA.
                                                                              PRT; 1276 AA
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 173-1276 FROM N.A.
                                                                            STANDARD;
1258 LLAQKGIYFSMVQA 1271
                                                                                                                                                                                                                                     NCBI_TaxID-10090;
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                                                                          MDR3_MOUSE
                                              RESULT 5
MDR3_MOUSE
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18;

81; Gaps

243

303 350 410 422 470 482

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us-09-882-694a-11.rsp

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GVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMS 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                991 APDYAKATVSASHIIRIIEKTPEIDSYSTQGLKPNMLEGNVQFSGFVFNYPTRPSIPVLQ 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVQQEPTLYQGSVRENVTLALEAEL--SEELCQGRLPARPMLWILSSLYQKALKRLAAQR 1156
                                                                                                                                                                                                                                                                         762 VISQVVTHRYQAAMFORVLDQDIELLDIPEQISGALTSQL-----SALPTQLQ 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQAAAQYLAY 978
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SEQUENCE OF 622-1276 FROM N.A.
MEDLINE-88122132; PubMed-2893255;
Endicott J.A., Juranka P.F., Sarangi F., Gerlach J.H., Deuchars K.L.,
                                                                                                                                                              655 GSSLIRRRSTRKSICGPHDQDRKLSTKEALDEDVPPASFWRILKLNSTEWPYFVVGIFCA 714
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MEDLINE-92135896; PubMed-1685679;
Endicott J.A., Sarangi F., Ling V.;
"Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
647 RPALERTHTTATSQAG--DLEKRKVPVGTLGYSLLKCILIMFYEQKNLYW-CFLLSTITV
                                                                                                                                                                                                                             704 LICAATFPGQALLFSRLLTVFELSG--HAAQERADFYILMFFVVALGNLVGYFTIGWTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 KAGEILTKRLRYMVFKSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGATGSRLAVIFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EL--ISANFLIYIVVGQHRLEQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNSSRDEARS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQ-----SF
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
NCBI_TaxID=10029;
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Multidarug resistance protein 2 (P-glycoprotein 2),
PGY2 OR PGP2.
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ID NRZ_CRIGR.
AC P21449
DT 01-NAY
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DC 
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                                              drug-sensitive Chinese hamster ovary cells.";
Mol. Cell. Blol. 7.4075-4081(1987).
1-1. Cell. Blol. 7.4075-4081(1987).
1-2. FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN WULTIDRUG-RESISTANT CELLS.
1-2. SUBCELLIARA LOCATION: Integral membrane protein.
1-3. FUNCTIONS FOR ISOSPORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SGASLPLMSIIFGSFTNKF--------NNYNSGDGSPEAFKADVDHFVLWF 101
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                                                                                                                                                                                                                                                                                -;- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
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                     "Simultaneous expression of two P-glycoprotein genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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ATP (POTENTIAL).
ATP (POTENTIAL).
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InterPro: IPR001439; ABC_transportr.
InterPro: IPR001687; APP_GTP_A.
Pfam: PF00664; ABC_membrane; 2.
Pfam: PF00005; ABC_tran; 2.
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1075
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                   QEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVL 281
178 VSKINDGIGDKIGMFFQSIATFLAAFIVGFISGWKLTLVILAVSPLIGLSSAMWAKVLTS 237
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Simultaneous expression of two P-glycoprotein genes in drug-sensitive Chinese hamster ovary cells.";
MOI. Cell. Biol. 7:4075-4081(1987).
-1. FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-1. SUBCELLALDAR LOCATION: Integral membrane protein.
-1. MISCELLANEOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
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MEDLINE-88122132; PubMed-2893255;
Endicott J.A., Juranka P.F., Sarangi F., Gerlach J.H., Deuchars K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Devine S.E., Hussain A., Davide J.P., Melera P.W.;
Full length and alternatively spliced pgp1 transcripts in multidrug-
resistant Chinese hamster lung cells.";
J. Biol. Chem. 266:4545-4555(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Chinese hamster P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                              Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Multigene family.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                            01-NAV-1991 (Rel. 18, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Multidury resistance protein 1 (P-glycoprotein 1).
ABCB1 OR PGY1 OR PGP1.
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EMBL, M19253; AAA37004.1; -.
EMBL, M1987; AAA37006.1; -.
PIR, A38696; DVHYIC.
InterPro; IPR001593; AAA.
InterPro; IPR00140; ABC_transporter_
InterPro; IPR001403; AAA.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PP00664; ABC_membrane; 2.
Pfam; PP00605; ABC_transportr.
SMART; SM00382; AAA; 2.
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Endicott J.A., Sarangi F., Ling V.
"Complete cDNA sequences encoding
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SEQUENCE FROM N.A.
MEDLINE-91154265; Pubmed-1671863;
STANDARD;
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NCBI_TaxID=10029;
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P21448;
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[2]
SEQUENCE OF 1-23 FROM N.A.
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44F3F92A186B4DFF CRC64;
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Kirschner L.S., Horwitz S.B.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS. MOUSE MDR? IS NOT CAPABLE OF CONFERRING DRUG RESISTANCE.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- NEUSCELLUAR LOCATION: Integral membrane protein.
--- RELATED BUT DISTINCT CELLULAR GENES.
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                                       SSGCGKSTVVQLLERFYDPMAGTVFLDGKEVNQLNVQWLRAHLGIVSQEPILFDCSIAEN
LLTVFELSGHAAQERAD - - FYILMFFVVALGNLVGYFTIGWTCNVISOVVTHRYQAAMFQ
                                                                                                                                                                       SMLRQDVSWFDNPKNTTGALTTRLANDAGQVKGATGARLAVITQNIANLGTGIIISLIYG
                                                                                                                                                                                                                                                      824 QHRLEQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRS
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                                                                                                                         RVLDQDIELLDIPEQISGALTSQLS------ALPTQLQELISANFLIYIVG
                                                                                                                                                                                                                                                                                                                  -----WQLTLLLLAIVP--11AIAGVVEMKMLSGQALKDKKELEGSGKIATEA----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Multidrug resistance protein 2 (P-glycoprotein 2).
PGY2 OR PGY-2 OR MDR2.
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ARSAANYILWLRTLKPTIRETE----ENKKKGPVGGCPVDLEDIEFRYRORDSARVLRG 1039
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                                                                                                              ERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNI----ANGFMDEQ 480
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321 ISKEYT-IGNAMTVFFSILIGAFSVGQAAPCIDAFANARGAAYVIFDIIDNNPKIDSFSE 379
                                                                     365 SGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLL
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenselsb-sib.ch).
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-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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InterPro; IPR003593; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
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           ROIRKIROKFFHAILRQEMGWFDIKGTTELNTRLTDDISKISEGIGDKVGMFFQAIATFF 200
                                                              SAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSI 244
                                                                                                                                                                 245 RTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAEWKGFRMY 304
                                                                                                                                                                                                                                                                 305 QNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKFTQLDPLDP 364
                                                                                                                                                                                                                                                                                                                                                                   365 SGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLL 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in oway modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isp-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                        Brown P.C., Thorgeirsson S.S., Silverman J.A.;
Cloning and regulation of the rat marz gene.";
Nucleic Acids Res. 21:3895-3891(1993).
-1- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED BRUG ACCUMULARION IN MULTIDRUG-RESISTANT CELLS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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                                                                                                              Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Rattus.
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16-OCT-2001 (Rel. 40, Last annotation update)
Multidrug resistance protein 2 (P-glycoprotein 2).
PGY2 OR MDR2.
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InfectPro; IRR003593, AAA.
InfectPro; IRR003409, ABG_Lrensporter_tmem.
InfectPro; IRR003439; ABG_Lrensportr.
InfectPro; IRR00439; ARD_GTP_A.
Pfam; PF00664; ABG_membrane; 2.
Pfam; PF00005; ABG_membrane; 2.
                                                                                                                                                                                                                                            STRAIN-FISCHER;
MEDLINE-93376516; PubMed-8103593;
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                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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PROSITE; PS00211; AGC_TRANS
ATP-binding; Glycoprotein;
Multigene family.
                                                                                      norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 VVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQLQ------ELISAN--- 815
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                                                                                                                                                           Query Match

24.6%; Score 1590.5; DB 1; Length 1281;
Best Local Similarity 32.4%; Pred. No. 3.1e-95;
Matches 421; Conservative 242; Mismatches 531; Indels 107; Gaps
                                                                                     SSSHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNK 76
                                                                                                                                                                                                                                                                                                                                                                                                              305 ONGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDP
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                                                                                                                        SISNOGRNKKKKVNLIGPLTLFRYSDWODKLFMLLGTIMAIAHGSGLPLMMIVFGEMTDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 = ramin, 1991).

FOUCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED FUNCTION: ENERGY-DEPENDENT EFFLUX.

SUBCELLULAR LOCATION: Integral membrane protein.

MISCELLARABOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A. Wheed-1685679; MEDLINE-92135896; PubMed-1685679; Endicott J.A., Sarangi F., Ling V.; Endicott J.A., sarangi F., Ling V.; "Complete CDNA sequences encoding the Chinese hamster P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY
                                                                                                                                                                                                       16-OCT-2001 (Rel. 40) Last annotation update)
Multidruy resistance protein 3 (P-glycoprotein 3).
EVY3 OR PGP3.
Critoctulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetiaee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00211; ABC_TRANSPORTER; 1,
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
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2203EF61EBB29602 CRC64;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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ATP (POTENTIAL).
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ATP (POTENTIAL).
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                     1233 STIQNADLIVVIDNGKVKEHGTHQQLLAQKGIYPSMVNIQA 1273
1219 STIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMCLAQS 1259
                                                                                                                                                             (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                               PRT; 1281 AA
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Interpro; IPR00140; ABC_transporter_tmem.
Interpro; IPR0014939; ABC_transportr.
Interpro; IPR001689; APC_fransportr.
Interpro; IPR001689; APC_fransportr.
Pfan; PF00664; ABC_membrane; 2.
Pfan; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00382; AAA; 2.
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HSSP; P13569; 1NBD.
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MDR3_CRIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- MISCELLANEOUS: IN MOUSE THE MDR CENE FAMILY INCLUDES THREE OR MORE RELATED BUT DISTINCT CELLULAR GENES.
-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                         1043 TIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQ 1102
                                                                            1159 QFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTSRTTIAVAHRL 1218
                                                                                                                                                                                           988 AANYILWLRTLKPTIRETE----ENKKKGPVGGCPVDLEDIEFRYRQRDSARVLRGVSM 1042
                           1005 SAAHLFSLFERQPLIDSYSGEGLWPDKFEG----SVTFNEVVFNYPTRANMPVLQGLSL 1059
                                                                                                                  1103 EPTLYQGSVRENVTLALEAEL-~SEELCQGRLPA--RPMLWILSSLYQKALKRLAAQRGM 1158
                                                                                                                                              1120 EPVLFDCSIAENIAYGDNSRVVSQDEIVRAAKAANIHPFIETLPOKY----KTRVGDKGT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTIE, PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                       1236 STIQNADLIVVIQNGKVKEHGTHQQLLAQKGIYFSMVNIQA 1276
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Multidarug resistance protein 1 (P-glycoprotein 1).
ABCBI OR PGYI OR MDRI OR MDRIB.
                                                                                                                                                                                                                                                                                                                                              PRT; 1277 AA.
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Interpro; IPR003593; AAA.
Interpro; IPR001140; ABC_transporter_tmem.
Interpro; IPR001439; ABC_transporter_tmem.
Interpro; IPR001687; AFP_GTP_A.
Pfam; PF00664; ABC_membrane; 2.
PF00005; ABC_tran; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                   167 TGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 FCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFG 346
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                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                         11 N-LINKED (GLCNAC, . .) (POTENTIAL).
141386 M-LINKED (GLCNAC, . .) (POTENTIAL).
141386 MM; BAFDDD619D2934C1 CRC64;
                                                                                                                                                                                                                               Query Match

24.6%; Score 1590; DB 1; Length 1277;
Best Local Similarity 31.7%; Pred No. 3.3e-95; Indela 148;
Matches 424; Conservative 254; Mismetches 510; Indela 148;
                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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741 MFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQ 800
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                                                                                                                                                                                                                                                                                           898 PCSPTVLGHVEQGLAKIIQ-----SFWFGRCFGFHLSQSMEFLAIALGFCIAVDNW 948
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Bykaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_FaxID-6239;
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MEDILINE-20085750; PubMed-1360540;
Lincke C.R., The I., van Groenigen M., Borst P.;
Lincke C.R., The Selycoprotein gene family of Caenorhabditis elegans. Cloning
"The P-91ycoprotein gene family of Caenorhabditis elegans. Cloning
and characterization of genomic and complementary DNA sequences.";
J. Wol. Biol. 228:701-711(1992).
                                                                                                                                                                       LASDASNVKGAMGSRLAV------VTONVANLGTG--IILSLVLVYGWQLTLL
                                                                                                                                                                                                                ------LPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRR
                                                                                                                                                                                                                                                                                                                               907 VVSLTREQKFETMYAQSLQIPYRNALKKAHVFGITFAF--TQAMIYFSYAA--CFRFGAY
                                                                                          LFLVMGMISFVTYFFQGFTFGKAGEILTKRLRYMVFKSMLRQDISWFDDHKNTTGSLTTR
                                                                                                                                     LSALPTOLOELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGCVWCTSTPAFGW----
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STRAIN-BRISTOL N2;
MEDLINE-93122700. N2;
Lincke C.R., Broeks A., The I., Plasterk H.A., Borst P.;
Lincke c.R., Broeks A., The I., Plasterk H.A., Borst P.;
The expression of two P-glycoprotein (pgp) genes in transgenic Caenorhabditis elegans is confined to intestinal cells.";
EMBO J. 12:1615-1620(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDR1_CAEEL STANDARD: PRT; 1321 AA. p34712; 1921 AA. 01-FEB-1994 (Rel. 28, Created) Ol-FEB-1994 (Rel. 28, Last sequence update) 16-OCT-1001 (Rel. 40, Last annotation update) Multidrug resistance protein I (P-glycoprotein A).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 QNYTKTD----FEHDVMNVVWSYAAMTVGMWAAGQIIVTCYLYVAEQMNNRLRREFVKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKL 197
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-i- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESIGFANT CELLS.
-i- SUBCELLIGLAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: INTESTINAL CELLS.
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVF
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11arity 30.9%; Pred. No. 1.2e-92;
Conservative 245; Mismatches 500; Indels 172;
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CTOPLASMIC (POTENTIAL).
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ATP-binding; Glycoprotein; Transmembrane; Transport;
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InterPro: IPR0013593; AAA.
InterPro: IPR00140; ABC_transporter_tmem.
InterPro: IPR001499; ABC_transportr.
InterPro: IPR001689; APC_Transportr.
InterPro: IPR001689; APC_Transportr.
InterPro: IPR001689; APC_Transportr.
InterPro: IPR001689; APC_Transportr.
InterPro: IPR001055; ABC_Transportr.
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                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Preryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                     Wu C.-T., Budding M., Griffin M.S., Croop J.M.; "Isolation and characterization of Drosophila multidrug resistance gene homologs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. ..) (POTENTIAL).
S -> N.
D -> N.
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Q00449;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Multidrug resistance protein homolog 49 (P-9lycoprotein 49).
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CYTOPLASMIC (POTENTIAL).
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InterPro: IPR001140; ABC_transporter_tmem.
InterPro: IPR001439; ABC_transportr.
InterPro: IPR001607; APC_Transportr.
InterPro: IPR001607; APC_Transportr.
Pfam; PP00064; ABC_membrane; 2.
Pfam; PP000054; ABC_tran; 2.
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PROSITE; PS00211; ABC_IRANSPORTER;
ATP-binding; Glycoprotein; Transmen
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MEDLINE-91304385; PubMed-2072901;
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Best Local Similarity
Matches 426; Conserv
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   YG-----CASSVLYLLNTCAYRMGLALIIDPPTMQPMRVLRVMYAITISTSTLGFATS 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962 SWAFCLPVQAAAQYLAYSTSFTKARSAANYIL-WLRTLKPTIRETEENKKKGPVGGCPVD 1020
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                                 KASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPK 556
                                                                                                                                                 AEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAA 616
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                                                                                                                                                                                                                                                                                LVTAQTFTDAVDSAAEGKFSRENSVARQTSEHEGLSRQASEMDDIMNRVRSSTIGSITNG 708
                                                                                                                                                                                                                                                                                                              --LEKRKVPVGTLGYSLLKCIL-----IMFYEQKNLYWCFL-LSTITVLICAA 708
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                                                                       LDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREKQMELVQKAC
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                                                                                    IS---AIRTTRILRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTV 177
                                                                                                                                                                          EEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAF 297
                                                                                                                                                                                               259 EEVFSGIRTVFAFSGQEKEKERFGKLLIPAENTGRKKGLYSGMGNALSWLIIYLCMALAI 318
                                                                                                                                                                                                                      WRGFRM-YQNGEVADVGKVFT-----VVLSVTLAATSISMLAPSGSVVYQRRIFGSELF 350
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                                                              79 VGVGTSSPAFALPMFGGGQQLTNASKEENNQAIIDDATAFGIGSLVGSVAMFLLITLAID 138
                                                                                                                                QALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLA 237
EGSISD-----YLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYN 81
                                                                                                                                                                                                                                                                                                                                                                    199 FLIMTFVIGIVSAFVYGWKLTLVVLSCVPFILAATSVVARLQGSLAEKELKSYSDAANVV
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              ------KADVDHFVLWFVYLFIGKFVLTYVSTAAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match | 22.8%; Score 1472.5; DB 1; Length 1321; Local Similarity 30.9%; Pred, No. 1.56-87; Score 1419; Conservative 234; Mismatches 530; Indels 171; Gaps
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ABIL_MOUSE STANDARD; PRT; 1321 AA.

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last sequence update)

Bile salt export pump (ATP-binding cassette, sub-family B, member 11)

ABCBIL OR BSEP OR SPGP.

Mus musculus (Mouse)

Musmalla: Euthera, Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBL_TaxID=10090;
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                                                                                                                                          LHEKAAREAAGERPALERTHTTA----TSQAGDLEKRKVPVGTLGYSLLKCILIMFYEQK
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                                                                                                                                                                               Indels 179; Gaps
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                                                                                                                                      1; Length 1321;
  N-LINKED (GLCNAC, . ) (POT
L -> P (IN REF. 2).
T -> V (IN REF. 2).
MW: 15B5EBE175D32967 CRC64;
                                                                                                                                   Query Match 22.7%; Score 1468.5; DB 1; Best Local Similarity 30.7%; Prof. No. 2.7e-97; Matches 417; Conservative 232; Mismatches 530;
125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROF entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedelsb-sib.ch).
                                                                                                                                                                                                  TISSUE-Liver;
MEDLINE-20076398; PubMed=10607905;
Green R.M., Hoda F., Ward K.L.;
"Molecular cloning and characterization of the murine bile salt export
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES, EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN ATP BINDING CASSETTE (ABC) DOMAIN.
SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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ATP (POTENTIAL).

ATP (POTENTIAL).

N-LINKED (GLCARC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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EMEL, AF133903; AAF14372.1;
EMEL, AF166815, AAD66419.1;
InterPro; IPR003593; AAA.
InterPro; IPR003593; AAA.
InterPro; IPR003493; AAC.
InterPro; IPR0016439; APC.
InterPro; IPR001647; APC.
InterPro; IPR001664; ABC.
InterPro; IPR00164; ABC.
InterPro; IPR00184; ABC.
INTERN; SM00182; ARA; 2.
PROSITE: PS00131; ARC.
ITRANSPORTER; 1.
AIP-binding; Transmembrane; Transport.
                                                                                                                                                               SEQUENCE OF 463-635 FROM N.A.
                                                                                                                                                                                     STRAIN-C57BL/6; TISSUE-Liver
                                                                                             pump.";
Gene 241:117-123(2000).
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930	79 338	1039 1098	)99 158	1158 1217	1218 1277	
DPDRLIFDSRRPCSPTVLGHVRQGLAKIJQSFWFGRCFGFHLSQ 	931 SMEFLAIALGECIAVDNMLQVSTTQLNFISSSWAFCLPVQAAAQYLAYS 979 :	TSFTKARSAANYILMLRTLKPTIRETEENKKKGPVGGCFVDLEDIEFRYRQRDSARVLRG   :     :	1040 VSMTIEPGQEVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSL 1099 :::::	VOQEPTLYQGSVRENVTLALEA-ELSEELCQGRLPARPMLWILSSLYQKALKRLAAQRGM 	QFSGGGRQRIAIARALIRNPKLLLLDEATSALDTGSERLVQAALDEASTSRTTIAVAHRL 	STIRNVDVIEVFANGRIAETGFHAELQRLRGRYYEMCL 1256   [  [   [   ]   ]
949	931	980	1040	1100	1159	1219
ço op	oy op	0y 0p	Qy Dp	Qy	oy pb	δλ

Search completed: April 27, 2002, 08:00:03 Job time:  $769\ \mathrm{sec}$ 

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

April 27, 2002, 07:48:23; Search time 68.15 Seconds (without alignments) 1780.790 Million cell updates/sec Run on:

US-09-882-694A-11 6455 I MADESEKPRPNQDGSESSSH......LQRLRGRYYEMCLAQSLDQA 1263 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ATES	Description		rocieta			multidrug resistan			multidrug resistan	multidrug resistan	multidrug resistan	-	P-qlycoprotein hom		p-qlycoprotein iso	p-qlycoprotein - r	ч	P-qlycoprotein-lik	P-glycoprotein-lik	hypothetical prote	probable ABC trans	multidrug resistan	hypothetical prote	•	hypothetical prote	probable P-qlycopr	probable P-qlycopr	multidruq resistan	probable ABC trans	
SUMMARIES	QI	4153	T43261	T30882	DVHU1	S55692	DVHU3	DVMS1	A34786	DVHY1C	DVMS2	T19982	T48007	S41646	148123	JH0502	E86155	D85023	T52319	T23476	T02187	827337	T21268	T04251	T22090	E85023	GB6404	A47377	F86155	•
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	Length	1362	1408	1307	1280	1287	1279	1276	1276	1276	1276	1294	1292	1278	1281	1277	1278	1229	1229	1321	1286	1321	1327	1233	1266	1230	1245	1283	1229	1
,	Query Match	30.5	27.7	27.6	25.6	25.5	25.4	25.3	25.2	25.0	24.8	24.8	24.7	24.7	24.6	24.6	24.6	24.1	24.1	24.1	24.1	24.0	24.0	23.9	23.7	23.6	23.6	23.6	23.5	
	Score	1970.5	1789.5	1780	1649.5	1648.5	1640.5	1630.5	1627.5	1611	1601.5	1601.5	1594	1592.5	1590.5	1590	1585.5	1556.5	1556.5	7	1553.5	1551	1549.5	7	1528.5	1525.5	1525	1523.5	21	,
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multidrug resistan	multidrug resistan	hypothetical prote	P-glycoprotein pgp	hypothetical prote	protein C34G6.4 [1	multidrug resistan	bile salt transpor	multidrug resistan	P-glycoprotein sis	probable P-glycopr	hypothetical prote	hypothetical prote	hypothetical prote	multidrug resistan	multidrug resistan
S30327	A41249	T22094	A42150	T21269	D87789	DVMS1A	T42842	T06165	T42228	F86405	T21267	H85202	T21266	530328	T30855
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1302 2	1302	1268	1286	1270	1289	1104	1321	1232	1321	1247	1291	1323	1318	1310	1254
•	'-,	` '		23.1 1270	, ,	•			• -	• •			• •		
•	23.4	` '	23.2		23.1	22.8	22.8	22.8	22.8	22.8	22.7	22.7	22.7	22.6	22.5

## ALIGNMENTS

Qy 111 LTYVSTAAITISAIRPTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQPGIA 170	Qy 51 IALICAIGSGASLPLMSIIFGSFTNKFNNYNSGDGSPEAFKADVDHFVLWFVYLFIGKFV 110	QY 9 RPNQDGSESSSHPPPEKETEGSISDYLRIFRYADKYDMTLNV 50 : 1 1	Ouery Match 30.5%; Score 1970.5; DB 2; Length 1362; Best Local Similarity 35.5%; Pred. No. 4.2e-133; Matches 484; Conservative 225; Mismatches 508; Indels 147; Gaps 24;	F,438-641/Domain: ATP-binding cassette homology <abc1> F,455-462/Region: nucleotide-binding motif A (P-loop) F,1137-1332/Domain: ATP-binding cassette homology <abc2> F,1154-1161/Region: nucleotide-binding motif A (P-loop)</abc2></abc1>	A;Gene: SPDB:SPCC663.03; pmd1 A;Map position: 3 C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homoloc;Keywords: ATP, glycoprotein; membrane protein; nucleotide binding; P-loop	A; Residues: 1-1333, 'TC', 1336-1362 <nis> A; Cross-references: EMBL:D10695; NID:g218549; PIDN:BAA01537.1; PID:d1002012; PID:g21</nis>	A; Reference number: S20548; MUID: 92244046 A; Accession: S20548	Mol. Microbiol. 6, 761-769, 1992 A/Tille: A leptomycian B resistance gene of Schizosaccharomyces pombe encodes a prote	A;Cross-references: EMBL:AL031307; NID:g3426126; PIDN:CAA20363.1; PID:g3426129; GSPD A;Experimental source: strain 972h.; cosmid c663  b:Nich: r · v-chida u · Nichimura u · Nichitau u · Nichitau u · v-chida u · Nichitau u · Nichitau u · v-chida u · Nichitau u · Nichitau u · v-chida u · Nichitau u · Nichitau u · v-chida u · Nichitau u · Nichitau u · v-chida u · v-c	A; Molecule type: DNA A; Residues: 1-1362 <see></see>	A; Reference number: 217318 A; Accession: T41534	RESULT 1	n B resistance protein, ABC transporter [imported] - fission yeast (Schizosa te names P-giyogorocein homolog : Schizosaccharomyces prome homolog : Schizosaccharomyces prome homolog : Schizosaccharomyces prome homolog on: "44134; S20548  K; Harris, D; Wood, V; Rajandream, M.A.; Barrell, B.G. ce number: 12134  Cen number: 12134  Cen number: 12134  Cen number: 12134  Cen number: 12136  Cen number: 12134  Cen number: 25248  Cen number: 12134  Cen nucleotide Dinding cassette proteins; ATP-binding cassette homology cABC2>  Comman: ATP-binding cassette homology cABC2>  Conservative 1225  Conservative 1225  Conservative 1225  Conservative 1225  Cen number: 12134  Cen nucleotide Dinding motif A (P-loop)  Cen number: 12134  Cen nucleotide Conservative 1225  Cen number: 12134  Cen nucleotide Conservative 1225  Cen number: 1211  Cen number: 1211  Cen number: 1211  Cen number: 1211  Cen nucleotide Conservative 1225  Cen number: 1211  Cen number: 1211  Cen nucleotide Conservative 1255  Cen number: 1211  Cen number: 1224  Cen number: 1224  Cen number: 1224  Cen number: 1224  Cen number: 12
PIDN:CAA20363.1; PID wa, M.; Nishiyama, M. osaccharomyces pombe  Troteins; ATP-binding nucleotide binding; anclop) P-loop) P-loop) P-loop I H H H H H H H H H H H H H H H H H H H	A, Reference number: 217318 A, Reference number: 217318 A, Reference number: 217318 A, Status: translated from GB/EMBL/DDBJ A, Holocule type: DNA A, Federal translated from GB/EMBL, ADBJ A, Holocule type: DNA A, Reference: EMBL.ALG31307; NID: 93426126; PIDN: CAA20363.1; PID: 93426129; GSPD A, Experimental source: strain 972h.; cosmid c663 A, Experimental source: strain 972h.; cosmid c663 A, Fisterence number: 520548; MUID: 92244046 A, Reference number: 520548 A, Reference number: 520548 A, Reference number: 520548 A, Reference strain a	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: 1-1362 < A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Residues: 1-1362 < A; Cross-references: EMBL:AL031307; NID:9244046 A; Mishi, K.; Yoshida, M.; Nishimura, M.; Nishiyama, M.; Hortinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:9244046 A; Reference number: S20548; MUID:9244046 A; Residues: 1-1333, TC', 1336-1362 <-NIS> A; Residues: 1-1333, TC', 1336-1362 <-NIS> A; Residues: T1-1333, TC', 1336-1362 <-NIS> A; Residues: PDBS: SPCC663.03; pmd1 A; Map position: S A; Gene: SPDB:SPCC663.03; pmd1 A; Map position: S C; Genetics: A; Gene: SPDB:SPCC663.03; pmd1 A; Map position: S C; Superfamily: unassigned ATP-binding cassette protein; nucleotide binding; P-loop B; A55-462/Region: nucleotide-binding motif A (P-loop) F; 1137-1332/Domain: ATP-binding motif A (P-loop) F; 1154-1161/Region: nucleotide-binding motif A (P-loop) F; 1154-1161/Region: nucleotide-binding motif A (P-loop) F; 1154-1161/Region: nucleotide-binding motif A (P-loop) F; 1164-1161/Region: nucleotide-binding mo	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: 1-1362 <-SEE> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Residues: 1-1362 <-SEE> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Rishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Accession: S20548; MUID:92244046 A; Molecule type: DNA A; Residues: 1-1333, TC', 1336-1362 <-NIS> A; Accession: S20548 A; Molecule type: DNA A; Residues: T1-1333, TC', 1336-1362 <-NIS> A; Gene: SPDB:SPCC663.03; pmd1 A; Molecule type: DNA A; Residues: Thining cassette protein; nucleotide binding; P-loop C; Genetics: A; Gene: SPDB:SPCC663.03; pmd1 A; Mpp position: 3 C; Superfamily: unassigned ATP-binding cassette homology <-ABCL> E; A85-462/Region: nucleotide-binding motif A (P-loop) E; 1137-1332/Domain: ATP-binding motif A (P-loop) E; 1154-1161/Region: nucleotide-binding motif A (P-loop)	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: 1.362 < SEE> A; Cross-references: EMBL:AL031307; NID:g3426126; PIDN:CAA20363.1; PID:g3426129; GSPD A; Experimental source: strain 922b.; cosmid c663 A; Experimental source: strain 92ab.; cosmid c663 A; Experimental source: strain 92ab.; is Nishiwaw, M.; Nishiyama, M.; Horinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Tile: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Accession: S20548; MUID:92244046 A; Accession: S20548 A; Molcoule type: DMA A; Residues: 1-1333, TC, 1336-1362 < NIS> A; Cross-references: EMBL:D10695; NID:g218549; PIDN:BAA01537.1; PID:d1002012; PID:g21 C; Genetics: A; Map position: 3 C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homoly C; Keywords: ATP; d1ycoprotein; membrane protein; nucleotide binding; P-loop	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: 1.1362 <see> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972b-; cosmid c663 A; Rishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Tile: A leptomyvin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Reference number: S20548; MUID:92244046 A; Residues: 1.1333, TC', 1336-1362 <nis> A; Residues: 1.1333, TC', 1336-1362 <nis> A; Residues: EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921</nis></nis></see>	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41524 A; Status: translated from GB/EMBL/DDBJ A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972+. cosmid c663 A; Reperimental source: strain 972+. i cosmid c663 A; Nishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Hyrinouchi, S Mol. Misrolo. 6, 761-769, 1992 A; Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Reference comber: S20548 A; Molecule troe: DNA	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1362 <-SEE> A; Residues: 1-1362 <-SEE> A; Cross references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972h-; cosmid c663 A; Experimental source: strain 972h-; cosmid c663 B; Nabli, K; Yoshida, M; Nishimura, M; Nishikawa, M; Nishiyama, M; Horinouchi, S A; Nishi, K A; Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote	A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DM A; Molecule type: DM A; Residues: 1-1362 <see> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972b.; cosmid c663 R; Nishi, K; Yoshida, M; Nishimura, M; Nishikawa, M; Nishiyama, M; Horinouchi, S</see>	A;Reference number: 217318 A;Accession: T41534 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1362 <see></see>	A; Reference number: 217318 A; Accession: T41534		leptomycin B resistance protein, ABC transporter [imported] - fission yeast (Schizosa N;Alternate names: P-glycoprotein homolog C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Arcesion: 741534: 520648	K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. to the EMBL Data Library, August 1998
R.Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  Ribbedger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  A, Reference number: 217318  A, Rocession: T41534  A, Status: translated from GB/EMBL/DDBJ  A, Rocession: T41534  A, Roleoute Type: DRA  A, Roleoute Type: DRA  A, Title: A leptomycin B resistance gene of Schizosacharomyces pombe encodes a prote A, Reference number: 220548; WUID:9244046  A, Miltol. K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Molloule Type: DRA  A, Ribib, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Molloule Type: DRA  A, Ribib, K.; Yoshida, M.; Mishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Molloule Type: DRA  A, Roleoule Type: DRA  A, References: EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921  C, Genetics: Tayayarotechen; membrane protein; nucleotide binding; P-loop  C, Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology cABC.)  C, Superfamily: unassigned ATP-binding cassette homology ABC.)  C, Superfamily: unassigned ATP-binding cassette homology ABC.)  C, Superfamily: unassigned ATP-binding cassette homology CABC.)  F, 138-61/Domain: MTP-binding cassette homology CABC.)  F, 137-133/Z/Domain: MTP-binding motif A (P-loop)  F, 1137-133/Z/Domain: MTP-binding motif A (P-loop)  F, 1137-133/Z/Domain: MTP-binding motif A (P-loop)  F, 1137-133/Z/Domain: MTP-binding motif A (P-loop)  P, 1137-133/Z/Domain: MTP-binding motif A (P-loop)  Ouery Match  Ouery Match  Best Local Similarity 35.5%; Pred No. 4.2e-133;  Matches 884; Conservative 225; Mismatches 568; Indels 147; Gaps 24;  Qy 9 RNDOGSESSBHPPEKER	R;Seeger, K; Hartis, D; Wood, V; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Reference number: 217318 A;Reference number: 217318 A;Reference number: 217318 A;Residues: 1-1362 < CSEE> A;Corsa references: EMBL:AL031307; NID:34426126; PIDN:CAA20363.1; PID:33426129; GSPD A;Experimental source: strain 972h - cosmid c663 A;Rossidues: 1-1362 < CSEE> A;Cross references: EMBL:AL031307; NID:3426126; PIDN:CAA20363.1; PID:33426129; GSPD A;Experimental source: strain 972h - cosmid c663 A;Rossidues: 1-1362 < CSEE> A;Accession: 5, 761-769, 1992 A;Title: A leptomycin B resistance gene of Schizosaccharcmyces pombe encodes a prote A;Reference number: S20548; MUID:92244046 A;Roccession: S30548 A;Roccession: S3	R.Seeger, K.; Harits, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMB1 Data Library, August 1998 A.Recession: T41234 A.Recession: T41234 A.Recession: T41234 A.Stetuus: translated from GB/EMB1/DDBJ A.Rocession: T41234 A.Rocession: T41234 A.Rocession: T41234 A.Rocession: T41234 A.Rocession: T41234 A.Rocession: T4124 A.Rocession: EMBL: AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A.Experimental source: strain 9234. A.Rocession: T761769, 1992 A.Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A.Reference number: S20548; MUID:92244046 A.Rocession: S20548 A.Molecule type: DNA A.Residues: 1-1333. TC'. 1336-1362 <nis> A.Cocession: S20548 A.Molecule type: DNA A.Residues: T-1333. TC'. 1336-1362 <nis> A.Cocession: S20548 A.Molecule type: DNA A.Residues: Multiple AMP-binding cassette protein: nucleotide binding cassette homology <abc1> C.Genetics: A.Gene: SPDE: SPCC63.03; pmd1 A.Map position: 3 C.Superfamily: unassigned Amp-binding cassette homology <abc1> F.485-467. Region: nucleotide-binding motif A (P-loop) F.485-467. Region: nucleotide-binding motif A (P-loop) F.1137-1332/Domain: APP-binding cassette homology SABC2&gt; F.1137-1332/Domain: APP-binding cassette homology SABC3&gt; Best Local Similarity 35.5%; Fred. No. 4.2e-133; Matches 484; Conservative 225; Mismatches 508; Indels 147; Gaps 24;</abc1></abc1></nis></nis>	R:Seceptr, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 A; Reference number: 21318 A; Reference number: 21318 A; Reference number: 21318 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1362 CSEE A; Cross rreferences: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: Stain 92h-; cosmid c663 A; Experimental source: stain 92h-; cosmid c663 A; Ribsh, K.; Yoshida, M.; Nishimura, M.; Nishiyama, M.; Horinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Title: A Leptomycin B resistance game of Schizosaccharomyces pombe encodes a prote A; Reference number: 520548; MUID:92244046 A; Reference number: 520548; MUID:92244046 A; Residues: 1-1333, TC, 1336-1362 <nis> A; Residues: 1-1333, TC, 1336-1362 <nis> A; Coss references: EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921 C; Genetics: A; Gene: SPDB:SPCC663.03; pmdl A; Map position: 3 C; Superfamily: unassigned ATP-binding cassette promology <abc1> E; 455-462/Region: nucleotide-binding motif A (P-loop) F; 1137-1332/Domain: ATP-binding motif A (P-loop) F; 1154-1161/Region: nucleotide-binding motif A (P-loop)</abc1></nis></nis>	R:Secret K: Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Reference number: 217318 A; Scession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Experimental Source: Strain 972h-; cosmid 663 A; Status: Mishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Mol. Mistobiol. 6, 761-769, 1992 A; Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: 520548; MUID:92244046 A; Molecule type: DMA A; Residues: 1-1333, 77C, 1336-1362 kMIS> A; Gross-references: EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921 C; Genetics: A; Gene: SPDB:SPCC663.03; pmd1 A; Map position: 3 costion: 4 costion: 4 costi	R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 A; Reference number: 21318 A; Reference number: 21318 A; Reference number: 21318 A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Status: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1.136 - SEES A; Cross references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: Status 922h-; cosmid c663 A; Experimental source: Status 922h-; cosmid c663 A; Ribsh, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Mol. Microbiol. 6, 761-769, 1992 A; Title: A Leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Accession: S20548 A; Residues: 1-1333, TC', 1336-1362 ANIS> A; Residues: 1-1333, TC', 1336-1362 ANIS> A; Residues: 1-1333, TC', 1336-1362 ANIS> A; Residues: 1-1333, TC', 1396-1362 ANIS> A; Corner, See February EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921	R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Accession: T41534 A; Returs: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1362 <see> A; Cross references: EMBL.AL031307; NID:g3426126; PIDN:CAA20363.1; PID:g3426129; GSPD A; Cross references: EMBL.AL031307; NID:g3426126; PIDN:CAA20363.1; PID:g3426129; GSPD A; Cross references: EMBL.AL031307; NID:g3426126; PIDN:CAA20363.1; PID:g3426129; GSPD A; Experimental source: strain 972h-; cosmid c663 A; Nishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S Mol. Microblol. 6, 761-769; J992 A; Title: A Leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Molecule type: DNA</see>	R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Accession: T41534 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1362 <sees 1992="" 6,="" 761-769,="" 972h-;="" a="" a;cross-references:="" a;experimental="" a;krossian="" a;microbiol.="" a;tille:="" at="" b="" c663="" cosmid="" downid="" embl.al031307;="" encodes="" fidn:caa20363.1;="" gene="" gspd="" leptomycin="" nid:93426126;="" of="" pid:93426129;="" pombe="" prote<="" resistance="" schizosaccharomyces="" source:="" strain="" td=""><td>R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. subnitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Rosidues: 1.1362 <see> A; Rosidues: 1.1362 <see> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972+.; cosmid c663 A; Experimental source: strain 972+.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S. R; Nishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S.</see></see></td><td>R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Rolecule type: DNA A; Residues: 1-1362 &lt; SEE&gt;</td><td>R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Reference number: 217318</td><td>R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998</td><td>leptomycin B resistance protein, ABC transporter [imported] - fission yeast (Schizosa N;Alternate names: P-glycoprotein homolog C;Species: Schizosaccharomyces pombe</td><td>3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 on: T41S34; S20548</td></sees>	R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. subnitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Rosidues: 1.1362 <see> A; Rosidues: 1.1362 <see> A; Cross-references: EMBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A; Experimental source: strain 972+.; cosmid c663 A; Experimental source: strain 972+.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S. R; Nishi, K.; Yoshida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S.</see></see>	R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Accession: T41534 A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Rolecule type: DNA A; Residues: 1-1362 < SEE>	R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A; Reference number: 217318 A; Reference number: 217318	R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998	leptomycin B resistance protein, ABC transporter [imported] - fission yeast (Schizosa N;Alternate names: P-glycoprotein homolog C;Species: Schizosaccharomyces pombe	3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 on: T41S34; S20548
C. Tate: 0.02 - 0.02    C. Accession: 74154, S2049 seaquence_revision 0.10c-1999 #text_change 02-Feb-2001  R. R. Seeger. K.; Harris, D.; Mood, V.; Rajandream, M.A.; Barrell, B.G.  B. Seeger. K.; Harris, D.; Mood, V.; Rajandream, M.A.; Barrell, B.G.  A. Accession: 741534  A. Accession: 761-76; 761-764  A. Experimental source: SMBL.AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD  A. Experimental source: SMBL.AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD  A. Experimental source: SMBL.AL031307; NID:9344046  A. Accession: 50264  A. Acc	C; Aster: 0.3-Dec-1999 #text_Cnange 0.2-Feb-2001 C; Aster: 0.3-Dec-1999 #text_Cnange 0.2-Feb-2001 R; Geegor, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. A; Gerencesion: T41334; S20548 A; Accession: T41334 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Accession: T41534 A; Status: translated from GB/EMBL/DDBJ A; Molecule Pype: DMA A; Residues: 1.136 < SEE A; Residues: Strain 972h-; cosmid c663 A; Residues: 1.136 < SEE A; Residues: 1.136 < SEE A; Residues: Strain 972h-; cosmid c663 A; Residues: 1.137 < SEE A; Title: A leptomycin B resistence gene of Schizosaccharomyces pombe encodes a prote A; Reference number: S20548; MUID:92244046 A; Reference number: S20548; MUID:92244046 A; Reference number: S20548; MUID:92244046 A; Reference number: S20548 A; Redidues: 1.133, "TC', 1336-1362 < NISS A; Residues: 1.133, "TC', 1336-1362 < NISS A; Residues: 1.133, "TC', 1336-1362 < NISS A; Residues: PRBC: D10695; NID:9218549; PIDN:BA01537.1; PID:d1002012; PID:921 C; Genetics: Conservation: membrane protein; nucleotide binding cassette homology < ABC:> C; Repyords: APP: 910cprotein; membrane protein; nucleotide binding cassette homology < ABC:> C; Repyords: APP: 910cprotein; membrane protein; nucleotide binding cassette homology < ABC:> F; 138-641/Domain: APP-binding cassette homology < ABC:> F; 1154-1161/Region: nucleotide-binding motif A (P-100P) F; 137-1332/Domain: APP-binding cassette homology < ABC:> C; Repyords: APP Conservative 225; Mismatches 508; Indels 147; Gaps 24; Matches 408; Conservative 225; Mismatches 508; Indels 147; Gaps 24; ABC: Called Conservative 225; Mismatches 508; Indels 147; Gaps 24; DB 37 KSENEASESHVUDVWRDPPEQPTPEQPEINTMOLIPARLSYADFWIDING.	Cybate: 0.2-Pec-1999 Feext_change 02-Peb-2001 Cybate: 0.2-Pec-1999 Feext_change 02-Peb-2001 Cybate: 0.2-Pec-1999 Feext_change 02-Peb-2001 Cybate: 0.2-Pec-1999 Feext_change 02-Peb-2001 Cybate: 0.2-Peb-2001 Cybate: 0.2-Pe	C. Caccesion: T41334; S20548 R. Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 R. Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. A. Reference number: 217318 A. Status: translated from GB/EMBL/DDBJ A. Reperlamental source: status 972h-; cosmid c663 A. Title: A leptomycin B resistance gene of Schizosaccharomyces pombe encodes a prote A. Reference number: \$20548; MUID:92244046 A. Accession: \$20548; MUID:92244046 A. Accession: \$20548 A. Molecule type: DMA A. Residues: 1-1333, 'TC', 1336-1362 kNIS> A. Cross -references: EMBL:D10695; NID:9218549; PIDN:BAA01537.1; PID:d1002012; PID:921656 encodes: SPB:SPCC663.03; pmd1 A. Molecule type: DMA A. Residues: 1-1333, 'TC', 1336-1362 kNIS> A. 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Chaccasion: T41134; S20548 R. Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the RMBL Data Library, August 1998 R. Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the RMBL Data Library, August 1998 A.; Reference number: 217318 A.; Status: T41534 A.; Status: T41534 A.; Status: Last Seeson and Cabe A.; Residues: 1.1362 A.; Status: Last Seeson and Cabe A.; Residues: Last Seeson and Cabe A.; Robert M.; Robida, M.; Nishimura, M.; Nishikawa, M.; Nishiyama, M.; Horinouchi, S. A.; Reference number: 220548; MUID:92244046 A.; Reference number: 220548; MUID:92244046 A.; Residues: 1.133, TC', 1336-1362 ANIS> A.; Residues: 1.133, TC', 1336-1362 A.; Residues: 1.1337, TC', 1336-1362 A.; Residues: 1.136-1362 A.; Residues: 1.13	C. Accession: T41534; S20548 R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. 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C;Accession: T41534; S20548 C;Accession: T41534; S20548 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Accession: T41534 A;Accession: T41534 A;Molecule type: DNA A;Residues: 1-1362 <see></see>	C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C; Accession: T41534; S20548 R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. subnited to the EMBL Data Library, August 1998 A; Reference number: 217318	C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C.Accession: T41534; \$20548 R.Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998	leptomycin B resistance protein, ABC transporter [imported] - fission yeast (Schizosa	te names: P-glycoprotein homolog : Schizosaccharomyces pombe
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Submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Residues: 1-1362 <see> A;Cross references: ERBL:AL031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A;Cross references: ERBL:Al031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A;Cross references: ERBL:Al031307; NID:93426126; PIDN:CAA20363.1; PID:93426129; GSPD A;Cross references: Sirain 972h-; cosmid c663 A;Cross references: Sirain 972h-; cosmid c663 A;Crobiol. 6, 761-769, 1992 A;Iitle: A Leptomycin B;resistance gene of Schizosaccharomyces pombe encodes a prote</see>	N.Aternate names: Fg-glycoptotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41534, 22054B R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 A;Recence number: 217318 A;Accession: T41534 A;Accession: T41534 A;Residues: translated from GB/EMBL/DDBJ A;Residues: 1-1362 <see 1-1362="" <see="" a;cross-references:="" a;residues:="" embl:al031307;="" gspd="" horinouchi,="" k.;="" m.;="" nid:g3426126;="" nishika<="" nishikawa,="" nishimura,="" nishiyama,="" pid:g3426129;="" pidn:caa20363.1;="" rishi,="" s.;="" td="" yoshiida,=""><td>N.Alternate names: Prglycoptotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41334, \$20548 R;Seeger, K; Harris, D; Wood, V; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 A;Recenson emuber: 217318 A;Accession: T41534 A;Accession: T41534 A;Accession: T41534 A;Keleuls: translated from GB/EMBL/DDBJ A;Residues: 1-1862 &lt;5EE&gt;</td><td>N.Alternate names: P-glycoprotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41534; S20548 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Accession: T41534</td><td>N.Alternate names: 'F-glycoptotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41534; 220548 B;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998</td><td></td><td>n B resistance protein, ABC transporter [imported] - fission yeast (Schizosa</td></see>	N.Alternate names: Prglycoptotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41334, \$20548 R;Seeger, K; Harris, D; Wood, V; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1998 A;Recenson emuber: 217318 A;Accession: T41534 A;Accession: T41534 A;Accession: T41534 A;Keleuls: translated from GB/EMBL/DDBJ A;Residues: 1-1862 <5EE>	N.Alternate names: P-glycoprotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41534; S20548 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998 A;Reference number: 217318 A;Accession: T41534	N.Alternate names: 'F-glycoptotein homolog C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001 C;Accession: T41534; 220548 B;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1998		n B resistance protein, ABC transporter [imported] - fission yeast (Schizosa

171 EKLVFTVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIY 230

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SAAYKESAAFACESTS --- AIRTVASLNREENVFAEYCDSLIKPGRESAIASLKSGLFFS 1026
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642
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                                  SRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIY 290
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multidrug resistance protein 1 - fungus (Filobasidium floriforme)
Cispecies: Filobasidialla neoformans, Cryptococcus neoformans
Cispecies: July 2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
Cispecies: July 2001 #sequence_revision: Tispecy, N.B.; Skatrud, P.L.
Gene 201, 21-29, 1997
A;Title: Cloning and characterization of CneMDR1: a Cryptococcus neoformans gene enc.
A;Reference number: Z22374; MUID:98072425
A;Reference number: Z22374; MUID:98072425
A;Reference number: Z22374; MUID:98072425
A;Reference number: Z22374; MUID:98072425
A;Residues: 1-1408 cTHO>
A;Residues: 1-1408 cTHO>
A;Residues: 1-1408 cTHO>
A;Cross-references: EMBL:U62929; NID:g2668552; PID:g2668553; PIDN:AAC49889.1
A;Experimental source: strain MI-106
Cigenetics:
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C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
C;Keywords: ATP; membrane protein; P-loop
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                                                                                                             1220 TIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMCLAQSLDQA 1263
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1319 SIQDADCIFVFDGGVIAEAGTHAELVKORGRYYELVVEQGLNKA 1362
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C.Soperfamly: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
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                                                                                                                                                                                           AAITISAIRITRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGKSTMYGLLERWYLPSSGRILLDGLELGQYNVKWIRSRIRLVQQEPVLFRGTIFQNIAN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTIVIAHKLATVKSAGNIA 591
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                                                                                                                   KPRPNQDGSESS----SHPPP----EKETEGSISDYLRIFRYADXYDWTLNVIALICA 56
                                                                                                                                               10 KPLPKSPGTGSTTTGHSVSHAEEVLDRQLHTPVSQIGFFGIYRYATRWDVAILFGSALAA
                                                                                                                                                                                                                                                                                    VOALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVL
                                                                                                                                                                                                                                                                                                           LTGLSTFVTAFIIAYIKNWKLALICSASLLALLLTMGGCSTLMLIFSKKALEYQGRGASM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 VISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHEKTLHEKAAREAAGERPALE
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                                                               tch 27.6%; Score 1780; DB 2; Length 1307; al Similarity 34.3%; Pred. No. 2e-119; and 466; Conservative 222; Wismatches 500; Indels 172; 466; Conservative 222; Wismatches 500; Indels 172;
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Cispecies: Aspergillus flavus
Cispecies: 22-0ot-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
CiAccession: T30882
Firobin, M.B.; Peerry, R.B.; Skatrud, P.L.
Gene 200, 11-23, 1997
A:Title: Genes encoding multiple drug resistance-like proteins in Aspergillus A:Reference number: 220917; MUID:98038972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Woleoule type: mRNA
A;Residuas: 1-1307 «TOB>
A,Cross-references: EMBL:G62931; NID:g2673946; PID:g2673947; PIDN:AABB8655.1
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1280 DANIYDFIVSLPDGFDTEVGGSGLGSGGRQRIATARALIRNFKVLLDDAYSALDSQS 1339
                                                                                                                                                                                                                                                                                                                                                                     GGYIRLKVVVLKDQRMKKLHAASAHLASEAAGAVKTVASLTREK-----DVRRIYSEALK 1050
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                             LQELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGC------VWCTSTPAF-- 853
                                                                                                                                                                                                                                                                                                                 950 VQGLFGPTLGTVV-----QSCATLI------GGCIIGLCYGPLLALIGIACIPILVS 995
                                                                                                                                                                                                                                                                                                                                             -GWL------PQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVL 904
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                                                                                           KLAQEAAAEALQVDDDIEDPDDAVFIGGSSPMQEKDKQLHRAVTGRSLASIAMDDIQAKR
                                                                                                                                                                                                                                  - NLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQ
                                                                                                                                                                                                                                                          FOSAGFSRAGWDLNGV-----LRKKLFTATLRHDIEWFDEERNSTGAVTSNLADQPQK
             ALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELI--EFGCHYAALVRAQ
                                                                                                                      640 AREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLS
                                                                                                                                               AEEVAGE----INTO---SSEGLYARLERMNSADKFIY---IIA
                                                                                                                                                                          700 TITVLICAATFPGQALLFSRLLTVFELSG-----HAAQERADFYILMFFVVALG----
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A;Reference nu
A;Accession: T
A;Status: prel
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A; McGealani A504,7; GB:J05168; NID:g187496; PIDN:AAA59576.1; PID:g386862
B; Kicka, N.; Yamano, Y.; Komano, T.; Deda, K.
A; Accession: PS0162
A; Accession: PS0162
A; McGeale type: DNA
A; Residues: 1-22 <KIO>
R; Kicka, N.; Yamano, Y.; Komano, T.; Ueda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Ueda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Miuka, N.; Yamano, Y.; Komano, T.; Orda, K.
S; Milacente type: DNA
A; Reference number: S1550
A; McGession: S1550
A; McGeala type: DNA
A; Residues: 1-22, K.
A; Coll 47, 381-389, 1986
A; McCession: C; Chin, J. E; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I.
Cell 47, 381-389, 1986
A; McCession: A5509;
A; McCession: 
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NiAlternate names: P-giycoprotein 1

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1990 #sequence_revision 18-Aug-1995 #text_change 19-Jan-2001

R;Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.

J. Biol. Chem. 265, $06-514, 1990

J. Biol. Chem. 265, $06-514, 1990

J. A;Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin

A;Recession: A34914.
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; Mestedie type: mRNA

; Fassidues: 1-184, 'V.'186-1280 <CH2>

; Chambers: T.C.': Pohl, 'J.' Glass, D.B.; Kuo, J.F.

; Chambers, T.C.': Pohl, 'J.' Glass, D.B.; Kuo, J.F.

; Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase in Reference number: 543838; MuID:94220047
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                                                                 932 TVVSLTMETEALQSYQAQLRRQLKSDILPIVKSSLL-----YASSQALPFFC
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A; Residues: 656-689 <CHA>
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C; Generios:

A; Generios:
A; Generios:
CDB:120712; OMIM:171050
A; Map position: 7921-7921
C; Superfamily: multidrug resistance protein: ATP-binding cassette homology
C; Keywords: ATP; duplication: 91ycoprotein; nucleotide binding: P-loop; phosphoproteil
C; Keywords: ATP; duplication: duplication
C; Keywords: ATP; duplication: duplication
F; 1638,653-1280,Region: duplication
F; 1638,653-1280,Region: hydrophila c4H1>
F; 31-67,Voomain: hydrophila c4H1>
F; 321-67,Voomain: hydrophila c4H1>
F; 321-55,Region: nucleotide-binding motif B
F; 521-55,Region: nucleotide-binding motif B
F; 51-55,Region: hydrophila c4H2>
F; 994-1280,Doomain: hydrophila c4H2>
F; 994-1280,Doomain: hydrophila c4H2>
F; 994-1280,Doomain: hydrophila c4H2>
F; 994-1280,Poomain: hydr
R;Gekeler, V.; Weger, S.; Probst, H.
Babchen. Blobbys. Bas. Commun. 169, 796-802, 1990
BATILLE: mdr1/P-gyvoprotein gene segments analyzed from various human leukemic cel.
BATILLE: mdr1/P-gyvoprotein gene segments analyzed from various human leukemic cel.
BASE ference number: 152238
BASE ference number: 152238
BASE ferences 152238
BASE ferences to DAN
BASE ferences: GBS M37724, NID:g183537; PIDN:AAA88047.1; PID:g553314
BASE ferences: GBS M37724, NID:g183537; PIDN:AAA88048.1; PID:g553314
BASE ferences: GBS M37725, NID:g183538; PIDN:AAA88048.1; PID:g553315
BASE ferences: GBS M37725, NID:g183538; PIDN:AAA88048.1; PID:g553315
CCOMMENT: This is an integral membrane protein overproduced in multidrug-resistant of Comment: This is an integral membrane protein overproduced in multidrug-resistant of Comment: This is
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multidrug resistance protein homolog (mdr) - African clawed frog
multidrug resistance protein homolog (mdr) - African clawed frog)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001
C;Accession: $55692
R;Castillo, G.; Shen, H.J.; Horwitz, S.B.
Biochim. Biophys. Acta 1262, 113-123, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 STAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 FTVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 VLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVIS
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                              703 VLICAATFPGQALLFSRLLTVFELSGHAAQERAD - FYILMFFVVALGNLVGYFTIGWTC
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A; Reference number: 138015; MUD:95200972
A; Accasion: 138015
A; Status: translated from GB/EMBL/DbBJ
A; Molecule type: mRNA
A; Residus: translated from GB/EMBL/DbBJ
A; Readus: translated from GB/EMBL/DbBJ
A; Readus: translated from GB/EMBL/DbBJ
A; Readus: 1.61, ReSSRVDLOAC' cRES.
A; Cross-references: EMBL:235284; MID:91006662; PIDN:CAA84542.1; PID:91006663
C; Comment: This is an integral membrane protein overproduced in multidrug-resistant tructurally and functionally unrelated lipophilic antitumor drugs.
C; Comment: This is an integral membrane protein overproduced in multidrug-resistant tructurally and functionally unrelated lipophilic antitumor drugs.
C; Genetics: GBB:120713; OMIN:171060
A; Map position: 7q21-7q21
C; Stoperfamily: multidrug resistance protein: uncleotide binding cassette homology cassette castofy cassette homology cassette homology cassette homology cassette homology cassette homology cassette homology cassette castofy cassette homology cassette hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 LNPGKILEBEMTRYAYYSGLGAGVLVAAYIQVSFWTLAAGROIRKIRQKFFHAILRQEI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 WHFDKQSNGALATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GWFDINDTTELNTRLTDDISKISEGIGDKVGMFFQAVATFFAGFIVGFIRGWKLTLVIMA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 VIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAOKKMVEKYDVF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 ISPILGLSAAVWAKILSAFSDKELAAYAKAGAVAEEALGAIRTVIAFGGONKELERYOKH 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPKAEK 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGAFSVGQAAPCIDAFANARGAAYVIFDIIDNNPKIDSFSERGHKPDSIKGNLEFNDVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 25.4%; score 1640.5; DB 1; Best Local Similarity 33.2%; Pred. No. 2.2e-109; Matches 422; Conservative 230; Mismatches 532;
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A; Residues: 1-1279 <VA1>
A; Residues: 1-1279 <VA1>
A; Residues: 1-1279 <VA1>
A; References: GB=Mu3334; NID:g187501; PIDN:AAA36207.1; PID:g307181
B; Van der Bliek, A, M.; Baas, F.; ten Houte de Lange, T.; Koolman, P.M.; van der Velde-Kq
EMBO J. 6, 3325-3331, 1987
A; Tille: The human mdr3 gene encodes a novel P-glycoprotein homologue and gives rise to
A; Reference number: S01346; MUID:88111519
A; Accession: S01346
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A; Residues: 1-1279 < LIN>
R; Smit, J.J.; Mol, C.A.; van Deemter, L.; Wagenaar, E.; Schinkel, A.H.; Borst, P.
B; Smit, J.J.; Mol, C.A.; van Deemter, L.; Wagenaar, E.; Schinkel, A.H.; Borst, P.
Blochim. Blophys. Acta 1261, 44-56, 1995
A; Title: Characterization of the promoter region of the human MDR3 P-glycoprotein gene.
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A Readidues: BS6-1034, FVDFGFO', 1094-1279 <VA2>
A Readidues: BS6-1034, FVDFGFO', 1094-1279 <VA2>
A CTOSS-references: EMBL:X06181; NID:934554; PIDN:CAA29547.1; PID:934525
R:Lincke, C.R.: Smit. J.J.M.; van der Velde-Koerts, T.; Borst, P.
A FILLE: Structure of the human MDR3 gene and physical mapping of the human MDR locus.
A Fielence number: A42213; MUID:91161629
A RACESSION: A2213
A Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLGAMALGQTSSFAPDYTKAMISAAHIPSLLERVPQIDSYSDQGEKPKNCSGNVVFRGVN 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1086 AEMSPRLYRGHMSLVQQEPTLYQGSVRENV-----TI-ALEAELSEBLCQG 1130
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                                                                                             814 AN-----FLIYIVVGQHRLEQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNSSRDEAR 866
                                                                                                                                                                                                                                                                                                                                                                                                         911 LAKIIQSFWFGRCFGFHLSQSMEFLAI-----ALGFCIAVDNWLQVSTTQLNFISSSWAF 965
                                                                                                                                                                     846 ONVANLGTAIIISFIYG-----WQLTLLILAIVP--VIAAAGLVEMKMFAGHAKKDKKE
                                                                                                                                                                                                                                                 867 SRKLGKLC ------RKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQG
                 786 GKAGEILTMRLRLGSFKSMLRQEIGWFDDSKNSTGALTTRLATDASQVQGATGTRLALLA
                                                                                                                                                                                                                                                                                                                             898 LEKACKISTDAVLNIRTVVSLTRERKFEAMYEKSLEGPYR-------
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A; Cross references: GB:M60348; NID:g199102; PIDN:AAA39513.1; PID:g554199
A; Croment: This is an integral membrane protein overproduced in multidrug-resistant c
C; Comment: This is an integral membrane protein overproduced in multidrug-resistant c
tructurally and functionally unrelated lipophilic antitumor drugs.
C; Genelics:
A; Gene: mdr1 (pgp1)
A; Introns: 21/2; 38/3; 92/1; 111/2; 175/2; 233/3; 274/2; 332/3; 370/3; 449/3;
C; Superfamily: multidrug resistance protein; APP-binding cassette homology
C; Keywords: AFP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane
F: 1-637, 653-1276/Region: quplication
F: 409-603/Domain: AFP-binding cassette homology <ABCl>
F; 550-554/Region: nucleotide-binding motif a (P-loop)
F; 1194-1198/Region: nucleotide-binding motif a
F; 73, 21,961.03/Finding site: AFP (Lys) #status predicted
F; 107/Binding site: AFP (Lys) #status predicted
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                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-21 <RES>
  A; Accession: 157510
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A; Residuces: 1.1276 cRAN-
A; Residuces: 1.1276 cRAN-
A; Residuces: 1.1276 cRAN-
A; Title: Mammalian multidrug resistance gene: complete cDNA sequence indicates strong
A; Title: Mammalian multidrug resistance gene: complete cDNA sequence indicates strong
A; A; A; Cacession: A25057
A; Accession: A25057
A; Medecule type: mRNA
A; Residuces: 1-1276 cGRO-
A; Residuces: GB-M14757; NID: 9199100; PIDN: AAA79005.1; PID: 9387426
B; Raymond, M.; Gros, P.
A; Raymond, M.; Gros, P.
A; A; A; C; Call-specific activity of cis-acting regulatory elements in the promoter of A; Reference number: 157510; MUJD: 91042535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multidrug resistance protein 1 - mouse
MyAlternate names: P-41-ycoprotein 1
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
R;Raymond, M.; Gros, P.
Proc. Natl. Acd. Sci. U.S.A. 86, 6488-6492, 1989
Proc. Natl. Acd. Sci. U.S.A. 86, 6488-6492, 1989
A;Pitle: Mammalian multidrug-resistance gene: correlation of exon organization with shacession: A33719;
A;Accession: A33719;
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                                            ----YSLLKCILIMFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFELSGHA
                                                                                 ANVPPVSFLKVLKL ---- NKTEWPYFVVGTVCAIANGGLQPAFSVIFSEIIAIFGPGDDA
                                                                                                                                A-QERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDI
                                                                                                                                                                                                                  PEQISGALTSQLSALPTQLQ-----ELISAN-----FLIYIVVGQHRLEQCSTTSL
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C;Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; 47406-600/Domain. APP-binding cassette homology AABCl> F;423-431/Region: nucleotide-binding motif A (F-loop) F;547-551/Region: nucleotide-binding motif A (F-loop) F;1049-1245/Domain: ATP-binding motif B (P-loop) F;1045/Domain: ATP-binding cassette homology AABCl> F;1056-1074/Region: nucleotide-binding motif A (P-loop) F;1057-1156/Region: nucleotide-binding motif B F;429/Binding site: ATP (Lys) #status predicted F;1072/Binding site: ATP (Lys) #status predicted
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Matches 419;
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(S.Species: Mus musculus (house mouse)
(S.Species: Musculus)
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A; Molecule types. mRNA
A; Roaldues: 1-1276
A; CDEV>
A; Residues: 1-1276
A; CDEV>
A; CROSS-references: GB:M30697; NID:g199111; PIDN:AAA39517.1; PID:g387429
B; HSU, S.I.H.; COhen, D.; Kirschner, L.S.; Lothstein, L.; Hartstein, M.; Horwitz, Mol. Cell. Biol. 10, 3596-3606, 1990
A; Title: Structural analysis of the mouse mdria (P-glycoprotein) promoter reveals A; Reference number: A35671; MUID:90287150
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                                                                                                      750 LVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQLQ 809
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosludes: 1-525, 'HV', 528-938,'S',940-1035,'V',1037-1276 <HSU>
A;Residues: 1-525,'HV',528-938,'S',990-1045,'V',1037-1276 <HSU>
A;Cross-references: GB:M3581; NID:9199404; PIDN:AAA39514.1; PID:9387427
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
       825 GAMGARLAV------VTQNVANLGTGVIL----SLVYGWQLTLLLVVIIPLIV
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A;Cross-references: EMBL:L03266
R;Tecter, LD.; Eckersberg, T.; Taal, Y.; Kuo, M.T.
Cell Growth Differ. 2, 429-437, 1991
A;Title: Analysis of the Chinese hamster P-glycoprotein/multidrug resistance gene ppp A;Reference number: 152823; MUID:92088970
A;Accession: 152823
A;Status: translated from GB/EMBL/DDBJ
A;Accession: 152823
A;Cross-references: GB:S81975; NID:9240862
C;Comment: This is an integral membrane protein overproduced in multidrug-resistant c tructurally and functionally unrelated lipophilic antitumor drugs.
C;Comentics:
A;Genetics:
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llarity 32.1%; Pred. No. 2.9e-107;
Conservative 251; Mismatches 534;
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es 413; Conserv
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Best Local S
Matches 413
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Nylternate names: P-91Vopportein pgp1
C:Species: Circetulus grisseus (Chinese hamster)
C:Deternate names: P-91Vopportein pgp1
C:Deternate names: P-91Vopportein pgp1
C:Deternate names: P-91Vopportein pgp1
C:Deternate names: P-91Vopportein pgp1
C:Deternate names: P-91Vopportein names: D-92 #text_change 19-Jan-2001
C:Deternate names: D-92Vopportein names: D-92 #text_change 19-Jan-2001
C:Accession: A38696; E38696; E38696; E38696; E331768; E5823
A:Accession: A38696; MulD:91154265
A:Accession: A38696; MulD:91154265
A:Molecule type: mRNA
A:Residues: 1-1276 cms.
A:Accession: C38666
A:Molecule type: mRNA
A:Residues: 108-1276 cms.
A:Accession: B38696
A:Molecule type: mRNA
A:Residues: 108-1276 cms.
A:Accession: B38696
A:Molecule type: mRNA
A:Residues: 1-32-771-1276 cms.
A:Accession: B38696
A:Molecule type: mRNA
A:Residues: 1-32-771-1276 cms.
A:Accession: B38696
A:Molecule type: mRNA
A:Residues: 1-32-771-1276 cms.
A:Accession: A.A:Juranda, P.F.: Sarangi, F.: Gerlach, J.H.: Deuchars, K.L.: Ling, V.
A:Title: Simultaneous expression of two P-9lycoprotein genes in drug-sensitive Chinese P:A:Accession: A2126
A:Accession: A
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Lochim. Biophys. Acta 1173, 303-313, 1993
Title: Structural and functional analysis of 5' flanking and intron 1 sequences
Reference number: $33768; MUID:93305724
Accession: $33768
                                                                                                                                                                                                                                                                                                             STSFTKARSAANYILWLRTLKPTIRETEENKKKGPVGGCPVDLEDIEFRYRQRDSARVLR 1038
                                                                                                                                                                                                                                                                                                                                                                   APDYAKATVSASHIIRIIEKTPEIDSYSTQGLKPNMLEGNVQFSGFVFNYPTRPSIPVLQ 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMOFSGGORQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTSRTTIAVAH 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 NIANLGTGIIISLIYG-----WQLTLLLLAIVP--IIAIAGVVEMKMLSGQALKDKKEL 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 706-1276 <END>
A;Cross-references: GB:MI7897; NID:9191158; PIDN:AAA37006.1; PID:9191159
                                                                                                                                                                                                                                                                                                                                                                                                                                    GVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GESEEVEKGQTLALVGSSGCGKSTVVQLLERFYDPWAGSVFLDGKEIKQLNVQWLRAQLG
                                                                                                                          EGSGKIATEA------IENFRTVVSLTREOKFETMYAQSLQIPYRNAMKKAH
                                                                                                                                                                                       WFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQAAAQYLAY
                                                                                                                                                                                                                               LVQQEPTLYQGSVRENVTLALEAEL -- SEELCQGRLPARPMLWILSSLYQKALKRLAAQR
                                                                   RKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-21 <2AS>
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Gaps

Length 1276;

244

379 424 439 480 498

184

540

547 600 959

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Signer mate:
Cisuperfamily: multidrug resistance protein; APP-binding cassette homology
Cisuperfamily: multidrug resistance protein; nucleotide binding; P-loop; transmembra
Fil-637,653-1276/Region: duplication;
Fi409-603/Domain: APP-binding cassette homology <ABGI>
Fi426-433/Region: nucleotide-binding motif A (P-loop)
Fi550-554/Region: nucleotide-binding motif B
Fi1049-1245/Domain: APP-binding motif A (P-loop)
Fi105-1106/Region: nucleotide-binding motif A (P-loop)
Fi105-1106/Region: nucleotide-binding motif B
Fi105-1106/Region: nucleotide-binding motif B
Fi38-34/Binding site: APP (Lys) *status predicted
Fi32/Binding site: APP (Lys) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 FNNYNSGDGS-PEAF-----KADVDHFVLWFVYLFIGKFVLTYVSTAAITISAI 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 ISKEYT-IGNAMIVFFSILIGAFSVGQAAPCIDAFANARGAAYVIFDIDNNPKIDSFSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 SGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 RDLPREKOMELVOKACKASNGDVFINELPNGYETEVGERAGALSGGORORIAIARSIISD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 KSLKSPHONRLDEETNELDANVPPV----SFLKVLKL----NKTEWPYFVVGTVCAIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFF
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  tructurally and functionally unrelated lipophilic antitumor drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1,
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NiAlternate names: P-glycoprotein MDR2
C;Species: Mus musculus (fouse mouse)
C;Accession: A30409; S7011
R;Gross, P.: Raymond, M.; Bell, J.; Housman, D.
R;Gros, P.: Raymond, M.; Bell, J.; Housman, D.
Mol. Cell. Biol. 8, 2770-2778, 1988
A;Title: Gloining and characterization of a second member of the mouse mdr gene family.
A;Reference number: A30409; MUID:88302195
A;Accession: A30409; MUID:88302195
A;Molecule type: mRNA
A;Residues: 1-1276 <-KBU>
A;Residues: A30409; MID:913253
A;Residues: Davo generation of simple sequence during gene amplification.
A;Reference number: S70711; MUID:96313253
A;Residues: A3-29 <-KRIS
A;Residues: A3-49 <-KRIS
A;Residues: A3-40 <-KRIS
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                                                                                          672 PHDQDRKLSTKEALDEDVPPISFWRILKLNSSEWPYFVVGIFCAIVNGALQPAFSIIFSK 731
                                                                                                                                                  LLTVFELSGHAAQERAD - - FYILMFEVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQ 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           884 SYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQ-----SFWFGRCFGFHLSQSMEF 934
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EKGIYFKLVMTQTAGNEIELGNEVGESKNEIDNLDMSSKDSAS---SLIRRRSTRRSIRG 671
                                                                                                                                                                                  RVLDQDIELLDIPEQISGALTSQLS------ALPTQLQELISANFLIYIVVG 823
                                                --DLEKRKVPVGTLGYSLLKCILIMFYEQKNLYW-CFLLSTITVLICAATFPGQALLFSR
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Superfamily: multidrug resistance protein: ATP-binding cassette homology
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submitted to the EMBL Data Library, April 1997
A.Reference number: 219853
A.Accession: T24202
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DMR
A.Residues: 1-1294 <- WIZ>
A.Status: Preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-1294 <- WIZ>
A.Status: Preliminary; translated from GB/EMBL/DDBJ
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A;Wolecule type: DNA
A;Rosidues: 1.1294 <WIL>
A;Cross-references: EMBL:281484; PIDN:CAB03973.1; GSPDB:GN00023; CESP:C47A10.1
A;Experimental source: clone C47A10
B;Basham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C47A10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T1998; T24202
R;Basham, V.
R;Basham, V.
A;Reference number: 219207
A;Accession: T19982
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                                                                                                                                                                                                                                                                                                                                          887 EAAGKIATEAIENIRTVVSLTQERKFESM-----YVEKLHGPYRNSVRKAHIYGIT 937
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VVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQLQ******ELISAN***
                                                                                                                                                            LSQSMEFLAIALGFCIAVDNWLQVSTTQLNF---ISSSWAFCLPVQAAAQYLAYSFTK
                                                   ----FLIYIVVGQHRLEQCSTTSLWMETGP----GGCVWCTSTPAFGWLPQNSSRDEARS
                                                                             LGTGIIISFIYG -----EMKMLAGNAKTAVAGIV-----EMKMLAGNAKRDKKEM
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972 AGARLVDDG---KTTFDSVFRVFFALTMAAVAISQSSSLSPDSSKASNAAASIFAVIDRE 1028
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841646
p-941646
p-91ycoprotein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Feb-2001
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                                                                                                                                                           RSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREKQMELVQKACKASNGDVFINELPN
                                                                                                                                                                                  511 GYETEVGERAGALSGGORORIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSK
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                                                                                                                                                                                                                                                                           629 QEHEKTLHEKAAREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGY------
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                                                                     AQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSSGRILLDGLELGQYNVKWL
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Nilternate names: protein T1713.110 [similarity] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (Mouse-ear cress)
C; Species: Arabidopsis thaliana (Mouse-ear cress)
C; State: T4800 | Sequence revision 20-Apr-2000 *text_change 18-Aug-2000
R; Risger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, Pebruary 2000
R; Risger on number: Z2448
A; Scession: T48007
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DAI
A; Residues: 1-1292 cRIE>
A; Ciscas-teferences: EMBL; A,138651
A; Experimental source: cultivar Columbia; BAC clone T17J13
C; Genetics;
A; Map position: 34, 142/1; 200/3; 354/2; 529/3; 621/1; 904/3; 989/3; 1077/3; 1175/3
A; Introns: 123/3; 142/1; 200/3; 354/2; 529/3; 621/1; 904/3; 989/3; 1077/3; 1175/3
C; Superfamily: multidrug resistance protein; ATP-binding cassette homology
F; 1066-1261/Domain: ATP-binding cassette homology <a href="https://domain.com/eng/app-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-ear-closs-
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                                                                  EEPRIDGMISSGTYPQLSG-EVKLNKVFFRYPERPAVPILQGLNVHVKPGQTLALVGPSG 1068
                                            CCKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTL 1117
                                                                                                                                                                                                                       1173 ALIRNPKLLLIDEATSALDTQSERLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFAN 1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.7%; Score 1594; DB 2;
ilarity 31.7%; Pred. No. 5e-106;
Conservative 260; Mismatches 492;
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                                                                                                                                                                                                                                                                                                             1233 GRIAETGTHAELQRLRGRYYEMCLAQSLDQA 1263
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 427; Conserv
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p-11/coprotein isoform III · Chinese hamster
[C.Species: Cricetulus griseas (Chinese hamster)
[C.Species: Cricetulus griseas (Chinese hamster)
[C.Datei 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Feb-2001
[C.Accession: 146123
[R.Endicott, J.A.; Sarangi, F.; Ling, V.
DNA Seq. 2, 89-101, 1991
[A.71Le: Complete cDNA sequences encoding the Chinese hamster P-glycoprotein gene fan A.71Le: Complete CDNA sequences for GB/EMBL/DDBJ
[A. Reference number: 148121; MUID:92135896
[A. Accession: 148123
[A. Status: preliminary; translated from GB/EMBL/DDBJ
[A. Residues: 1-1281 FRES>
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                                                                                                                                                                                                                                       724 QPAFSIILSEMIAIFGPGDDTVKQQKCNMFSLVFLGLGVHSFFTFFLQGFTFGKAGEILT 783
                                                                                                                                                                                                                                                                                                                                                                                                           -FLIYIVVGQHRLEQCSTTSLWMETGP----GGCVWCTSTPAFGWLPQNSSRDEARSRKL 870
                                                                                                           668 KSLKSSRAHONRLDVETNELDANVPPVSFLKVLRL----NKTEWPYFVVGTLCALANGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKIATEAIENIRTVVSLTQERKFESM------YVEKLHGPYRNSVRKAHIYGITFSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988 AANYILWIRTIKPTIRETEE-----NKKKGPVGGCPVDLEDIEFRYRQRDSARVLRGVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1043 TIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1103 EPTLYQGSVRENVTLALEAEL- SEELCQGRLPA--RPMLWILSSLYQKALKRLAAQRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1117 EPILEDCSIAKNIAYGDNSRVVSQDEIVRAAKEANIHPFIETLPQKYETRV----GDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAALDEASTSRTTIAVAHRL
                                                                   ATSOAG-----DLEKRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLSTITVLICAAT
                                                                                                                                                                                                                                                                                                                                                      784 TRLRSMAFKAMLRODMSWFDDHKNSTGALSTRLATDAAQVQGATGTRLALIAQNTANLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 944 GIIISFIYG-----WOLTLLLSVVPFIAVAGIV-----EMKMLAGNAKRDKKEMEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQ
                                                                                                                                                                                                                                                                                                   769 HRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQLQ-----ELISAN----
          OGSHSELIKKEGIYFRLVNMQTSGSQ1LSEEFEVELSDEKAAGGVAPNGWKARIFRNSTK
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24.6%; Score 1590.5; DB 2;
Best Local Similarity 32.4%; Pred, No. 9.8e-106;
Matches 421; Conservative 242; Mismatches 531;
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C; Accession: $41646; S22354
R; Brown, P.C.; Thorgeirsen, S.S.; Silverman, J.A.
Nucleic Acids Res. 21, 3865-3891, 1993
A; Title: Cloning and regulation of the rat mdr2 gene.
A; Reference number: $41646; MUID:93376516
A; Accession: $41646
A; Accession: $22351, MUID:9310192; PIDN:AA02937.1; PID:9310193
A; Chockim: Biophys, Acta 1130, 157-165, 1992
A; Title: Identification of distinct P-91ycoprotein gene sequences in rat.
A; Reference number: $22351, MUID:92223089
A; Chockim: Brown accession: $22351, MUID:92223089
A; Chockim: Brown accession: $411-1278
A; Accession: $121-1278
A; Chockim: Arp-binding cassette homology Acadiant Arp-binding cassette homology Acadiant Arp-binding cassette homology Acadiant Arp-binding cassette homology Acadiant Arp-binding motif A (P-100p)
F; 1051-1247/Nomain: Arp-binding motif A (P-100p)
F; 1051-1247/Nomain: Arp-binding motif A (P-100p)
F; 1068-1075/Region: nucleotide-binding motif A (P-100p)
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24.7%; Score 1592.5; DB 2; Length
Bast Local Similarity 32.4%; Pred; No. 6.58-106;
Matches 422; Conservative 243; Mismatches 529; Indels
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                                                                                                    125 RTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFF 184
                                                                                                                                                                                                                       673 LKSSRAHHHRLDVDADELDANVPPV----SFLKVLKL----NKTEWPYFVVGTVCAIVN 723
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                                                                                                                                                                                                                                                         305 QNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDP 364
                                                                                                                                                                                                                                                                                                            SGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLL 424
                                                                                                                                                                                                                                                                                                                                                                          485 REKQMELVQKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKIL 544
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                                                 77 FNNYNSGDGS-PEAF-----KADVDHFVLWFVYLFIGKFVLTYVSTAAITISAI 124
                                                                                                                                                                                                                                                                                                                                                             ERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLP 484
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                                                                                                                      605 HELIEFGCHYAALVRAQDLGAD-EQOEHEKTLHEKAAREAAGERPALERTHTTATS----
17 SSSHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNK
                      25 SISNQGRNKKKKVNLIGPLTLFRYSDWQDKLFWLLGTIMAIAHGSGLPLMMIVFGEMTDK
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A.Fitle: Cloning and characterization of a member of the rat multidrug resistance (md A.Fitle: Cloning and characterization of a member of the rat multidrug resistance (md A.Feference number: JH0502; MUID:92039081

A.Molecula type: mRNA
A.Molecula type: mRNA
A.Fesidues: 1-1277 ASIL>
A.Feferences: GB:M62425
R.Deuchars, K.L.; Duthle, M.; Llng, V.
B.Jochim: Blophys: Acta 1120, 157-165, 1992
A.Feference number: 522351; MUID:92223089
A.Feference number: 522351; MUID:92223089
A.Accession: 522353
A.Molecula type: DNA
A.Feferences: EMBL:X61104; NID:956890; PIDN:CAA43416.1; PID:91334219
A.Fecession: 522352
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A/ACCESSION: 242-222
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A/Molecule type: DNA
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                                                                                1103 EPTLYQGSVRENVTLALEAEL - SEELCQGRLPA - RPMLWILSSLYQKALKRLAAQRGW 1158
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Cispeciaes: Rattus norvegicus (Norway rat)
Cibate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
Cibates 31-Mar-1992 sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
Cibates 31-Mar-1992 sequence_revision 31-Mar-1992 #text_change 02-Feb-2001
Risilvermann J.A.: Raunio, H.; Gant, T.W.; Thorgeirsson, S.S.
Gene 106, 229-236, 1991
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                                                 287 FCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFG 346
                                                                                                                                           347 SELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKT 406
                                                                                                                                                                                         407 TALVGASGSGKSTMYGLLERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRG 466
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                                                                                TRIYSRAAVLAEEVLSSIRTVHAFYAOKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEY
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: April 27, 2002, 07:58:40; Search time 24.91 Seconds

(without alignments)
354.654 Million cell updates/sec

1 MADESERPRPNDOSSESSH........LORLRGRYYEMCLAQSLDOA 1263

Sequence: 1 MADESERPRPNDOSSESSH.........LORLRGRYYEMCLAQSLDOA 1263

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 40831 seqs, 6994805 residues

Total number of hits satisfying chosen parameters: 40831

Minimum DB seq length: 0

Maximum Match 100*

Post-processing: Minimum Match 00*

Isting first 45 summaries

Database: Pending-Patents.AA.New:*

1. Cgn2_6/ptodata/Z/pbaA/US06_NEW_COMB.pep:*

2. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*

3. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*

4. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*

4. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/Z/pbaA/US08_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ion	Sequence 2, Appli Sequence 1211, Ap Sequence 1211, Ap Sequence 1215, Ap Sequence 1015, Ap Sequence 1015, Ap Sequence 6188, Ap Sequence 6291, Ap Sequence 6291, Ap Sequence 6190, Ap Sequence 6190, Ap Sequence 6190, Ap Sequence 6190, Ap Sequence 6190, Ap Sequence 6291, Ap Sequence 6261, App Sequence 6261, App Sequence 6261, App Sequence 6261, App Sequence 6261, Ap
SUMMARIES	PCT US02 -07826 - 2 US-10-573 -655B 11231 US-09-573 -655B 11231 US-09-574 -655B 11231 US-09-574 -655B 11231 US-09-574 -655B 11015 US-09-574 -655B 1014 US-09-574 -655B 1014 US-09-574 -620B 6188 US-09-540 -209B 625 US-09-540 -209B 625 US-09-540 -209B 625 US-09-540 -209B 625 US-09-573 -655B -2417 US-09-574 -655B -2417 US-09-574 -209B 1134 US-09-574 -209B 1135 US-09-574 -209B 1135 US-09-574 -209B 1135 US-09-574 -209B 1135 US-09-574 -209B 1135 US-09-574 -209B 6756 US-09-540 -209B 6756
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& Query Match	44114668887777777
Score	1640 1640 1640 1640 1640 1640 1640 1640
Result No.	11004000800110040011004001100400

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APPLICANT: School E. NOTALS
APPLICANT: School E. NOTALS
APPLICANT: School E. NOTALS
APPLICANT: Ami SEN
APPLICANT: Ami SEN
APPLICANT: Peter OLANDT
APPLICANT: Peter OLANDT
APPLICANT: Peter VEIBY
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APPLICANT: Rosemarie SchMANDT
APPLICANT: Rosemarie SchMANDT
APPLICANT: Rosemarie SchMANDT
APPLICANT: Rosemarie SchMANDT
APPLICANT: Raren GLATT
TITLE OF INVENTION: NUCLEIC Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: NUBER: 05/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR PPLICATION NUBBER: 60/276,025
PRIOR PPLICATION NUBBER: 60/276,025
PRIOR APPLICATION NUBBER: 60/235,149
PRIOR PPLICATION NUBBER: 60/236,0325,149
PRIOR PPLICATION NUBBER: 60/236,036
PRIOR PPLICATION NUBBER: 60/2324,967
PRIOR PPLICATION NUBBER: 60/2324,967
PRIOR PPLICATION NUBBER: 60/2325,102
PRIOR PILING DATE: 2001-09-16
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
129 TLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFV 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overy Match 25.4%; Score 1640; DB 6; Best Local Similarity 32.3%; Pred. No. 4.2e-119; Matches 428; Conservative 243; Mismatches 489;
                                                                                                                                                                                                                Sequence 2, Application US/10097340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Manjula GANNAVARAPU
Sebastian HOERSCH
Shubhangi KAMAYKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                                                                                                                                                                                                            APPLICANT: JOHN MONAHAN APPLICANT: Maniula GANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-2
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                                                                                                         1271 SVOA 1274
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  189 VALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVH 248
                                         206 VGFTRGWKLTLVILAISPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVI 265
                                                                                     249 AFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGE 308
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                                                           309 VADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQ
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Sequence 1211. Application US/09573655B
GENERAL INFORMATION:
GENERAL INFORMATION:
THORMATICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
TITLE OF INVENTION: Thereby
FILE OF INVENTION: Thereby
FILE REFERENCE: 2760-0876P
CURRENT APPLICATION UNMER: US/09/573,655B
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 2281
SOFTWARE: Patentin version 3.0
SEQ ID NO 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
1211 KVVQEALDKAREGRICIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSMV 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LEEVSETKROKEEEEEEVKKTEKKDEEHEKTKTVPFYKLFAFADSFDFLLMILGTLGSIGN 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
24.1%; Score 1553.5; DB 5;
Best Local Similarity 30.2%; Pred. No. 2.1e-112;
Matches 401; Conservative 264; Mismatches 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana
US-09-573-6558-1211
                                             1256 LAQS 1259
                                                                                                                                                           RESULT 3
US-09-573-655B-1211
                                                                                      SVQA 1274
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RESULT 6
US-09-573-655B-1015
US-09-573-655B-1015
Sequence 1015, Application US/09573655B
SENERAL INFORMATION:
TAPLICANT: SOLCOVIVEV, Victor and TROUKHAN, Maxim
TILLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TILLE OF INVENTION: Thereby
TILLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/573,655B
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: Patentin version 3.0
SEQ ID NO 1015
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                                   70 PNODOTKTAS----SKKILRTISSYLWM---KDNPELRFRVIAALACLIGAKFLNVOVPF 122
             DEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHE 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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8.5%; Score 546.5; DB 5;
Best Local Similarity 28.2%; Pred. No. 9.5e-35;
Matches 181; Conservative 122; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-1015
                                                                                                                     596 LLAKNGYYRLUNDMÓSL 612
                                                                                     LIEFGCHYAALVRAQDL
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SEQUENCE STATE OF TWORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FIRE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/540,209B
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 6953
LENGTH: 612
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                                                                                                                                           PEAFKADVDHFVLWFVYLFIGKFVLT-----YVSTAAITISAIRT--TRTLRRVFLECT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRLPLGFFSEERKGDIJARMSGDVGEIENSVTSSLDMLVKNPILLIAYFTTLLVISWQLT 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 KYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFLKCSNEFRDATNKVATRQALAHPMSEFLGTTMIVIVLWFGGSLILSSHSSIDASTFMV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 VLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLD-------PSG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 YLTILY----SVINPLKEFSKAGYNIPKGLASMERVDKILKAENKIVEIPNP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 KQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLER 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPRE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 KOMELVOKACKASNGDVFINELPNGYETEVGERAGALSGGORQRIAIARSIISDPKILLL 546
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                                                                           1088 KDIRKYNLKAIRKHIAIVPQEPCLFGTTIYENIAYGHECATEAEIIQAATLASAHKFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GSFTNKFNNYNSGDGS
                                                 1083 ENIAEMSPRLYRGHMSLVQOEPTLYQGSVRENVTLALEAELSEELCQGRLPARPMLWILS
                                                                                                                     1143 SLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSERLVQAAL
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                                                                                                                                                                                           1203 DEASTSRITIAVAHRLSTIRNVDVIFVFANGRIAETGTHAEL 1244
                                                                                                                                                                                                               / Match 10.6%; Score 682.5; DB 5; Local Similarity 30.6%; Pred. No. 2.3e-45; nes 189; Conservative 104; Mismatches 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) TYPE: PRT
; ORGANISM: B.fragilis
US-09-540-2098-6953
                                                                                                                                                                                                                                                                                 SULT 5
.09-540-209B-6953
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Matches
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Sequence 1014, Application US/09573655B
GENERAL INFORMATION:
SIGNATION:
TILLE OF INVENTION: SOCIONYEY, VICTOR and TROUKHAN, MAXIM
TILLE OF INVENTION: SHOWN SEQUENCE-DETERMINED DNA FRAGMENTS and Corresponding Polypept
TITLE OF INVENTION: Thereby
TITLE DF INVENTION: Thereby
TITLE OF INVENTION: 10876P
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: Patentin version 3.0
SEQ ID NO 1014
LENGTH 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                69 STSTSAPHPEKINRTSSENILRMI---SSYLWMKDNPKICFRVISAFACLVGA----- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 QPEGCL--GQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLE 425
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                                                                                                                                                                                                                                                                                                                                                                  Indels 139;
                                                                                                                                                                                                                                                                                                                             Length 1123;
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                                                                                                                                                                                                                                                       ; ORGANISM: Arabidopsis thaliana
US-09-573-6558-1014
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    JS-09-573-655B-1014
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US-10-102-806-726
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                                                                                                                                                        APPLICANT: GATY I. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NOS: 10444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 YMERPINDYI----EPGDFQGLV-RILLFLAAIYLTGVAATYIEYILLNKIGQRIVTRM 178
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582 ATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQD 622
                    Query Match
8.4%; Score 544.5; DB 5;
Best Local Similarity 27.8%; Pred. No. 1.3e-34;
Matches 175; Conservative 118; Mismatches 269;
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                                                                                                                           Sequence 6188, Application US/09540209B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: B.fragills
US-09-540-209B-6188
                                                                                        RESULT 7
US-09-540-209B-6188
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LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (690)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 SMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 VRGLCLLGIMLWGSVSLTMYTLITLPLLFLLPKKVGKWYQLLEVQVRESLAKSSQVAIEA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION:
FILE REFERENCE: PAIJOPLCI
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US/10/102,806
PRIOR APPLICATION NUMBER: OS/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PREGETIN Ver. 2.0
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OTHER INFORMATION: Xaa
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Sequence 6291, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILMS DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 6291
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                                                                                                                                                                                                                                                                                                                                                                                                                  25 KETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYNSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 EVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 FRMYQNGEVADVGKVFTVVLSVTLAATSI -- SMLAPS-GSVVYQRRIFGS-----ELFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILLMONDS------RSLTLAAVWLFFIILGPGVASPVYKLMYLGSSTREINEGVS
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                                                                                                                                                                                                                                                                                                                                                         Length 608;
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             521 GALSGGORQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEAL
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US-09-540-209B-6291
                                                                          RESULT 10
US-09-540-209B-6291
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Sequence 5749, Application US/09540209B
SEGUREAL INFORMATION:
APPLICANT; Gary L.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDE
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001.
CURRENT APPLICATION NUMBER: US/09/540,209B
SEQ ID NOS: 10444
SEQ ID NOS: 10444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 QG-MLPFISKAVIDVGITTSDRNFINM-----VLIGNICILLSVMFFNVLRDWILLHI- 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 27.6%; Score 490; DB 5; Length 735; Similarity 27.6%; Pred. No. 2.6e-30; Conservative 117; Mismatches 253; Indels 110;
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10-09-540-209B-6190

1 Sequence 6190, Application US/09540209B

2 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: B.fragilis
US-09-540-209B-5749
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Best Local Simi
Matches 183;
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                                                  Sequence 8625, Application US/09540209B
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
FILE REPERBNCE: 2709-1001-001
CURRENT APPLICATION NUMBER: 02/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 8625
LENGTH: 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 -WQWERIQVKLEKISVKGLAL---CQVQQVGSVFFNQTTNIVISFIAAKSVVEGNMTLGM 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEYFCIYAAIALAFWKGFRMYQNGEVADVGKVF----TVVLSVTLAATSISMLAPSGS 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREKQMELVQKA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 KIGETPLDVVNPHLWRAKSGSVMQDGFILSDTIANNIAVG--EEQVDVER-----FRHA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDP 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SEKPRPNQDGSESSSHPPPEKETEG----SISDYLRIF-RYADKYDWTLNVIALICAIGS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVYQRRIFG---SELFSIIDKPTQLDPLDPSGKQPEGCLGQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 7.7%; Score 498; DB 5; Length 740; Best Local Similarity 27.3%; Pred. No. 6.2e-31; Matches 183; Conservative 111; Mismatches 263; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASLPLMSIIFGSFTNKFNNYNSGDGSPEAFKADVDHFVLWFVYL---
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                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: B.fragilis
US-09-540-209B-8625
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US-09-540-209B-5749
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Sequence 4, Application US/10076157

Sequence 4, Application US/10076157

GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Suchberger, Harald
APPLICANT: Josefus Maria Molfgang
APPLICANT: Jimenez, Alberto:
APPLICANT: Jimenez, Alberto:
APPLICANT: Jimenez, Alberto:
TITLE OF INVENTION: Genes of purine blosynthesis from Ashbya Gossypli and the ITTLE OF INVENTION: in
TITLE OF INVENTION: microbial riboflavin synthesis
FILE REFERENCE: 486481V
CURRENT APPLICATION NUMBER: US/10/076,157
                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 TNGSGLSQGQKQKILIARAIXKNPDFIPLDEAFNSLDTNNEKQISKNLETILEGKTAIVI 692
                                                                                                                                                                                                HNMNEMETRASFSHFMKYLKPHHRYLGQV-IVGMVAGILIGLLSPFIS-----OSIVD 210
                                                                                                                                                                                                                                                                     134 --FLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEK-----LVFTVQALSMF 183
                                                                                                                                                                                                                                                                                                                                                F---SAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                         318 XXESNMFLVFMIGN-----TVYTGWIFLFLKQRKKLDNQLFGCRATNQNDL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 EYFCIYAAIALAFWKGFRM---YQNGEV-ADVGKVFTVVLSVTLAATSISMLAPSGSVVY 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR--RIFGSELFSIIDKPTOLDPLOPSGKQPEGCLGQIEIQNLAFAYPSRPSA-QVLRDF 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 EEEPEISESKVSIPIEK------GVKVKDLDEYY--NPNLNKVLDNI 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 NLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSSGRILLDGLELGQYNVKWLRSRIRLV 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 QQEPVLFRGTIFQNIANGFMDEQRDLPREKOMELVQKACKASNGDVFINELPNGYETEVG 517
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                                                                                                                                                                                                                                           80 YNSGDGSPEAFKADVDHFVLWFV-YLFIGKFVLTYVSTAAITISAIRTTRILRRV---- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LSSIRTVHAF----YAQKKM----VEKYDVF-----LQQAHQEGKKKSPNNGVLFST 284
                                                                                                                       Gaps
                                                                                                                                                             20 HPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNN 79
                                                                             Query Match
7.1%; Score 457; DB 5; Length 740;
Best Local Similarity 26.4%; Pred. No. 9.30-28; Indels 108;
Matches 170; Conservative 115; Mismatches 251; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 AHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQ 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR PILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 09/212,247
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: WORDER:
  ; ORGANISM: B.fragilis
US-09-540-209B-8427
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US-09-540-209B-8427
Sequence 8427, Application US/09540209B
Sequence 8427, Application US/09540209B
Sequence 8427, Application US/09540209B
September 1 Nucleus Sequence 8427, Application US/09540209B
Settle Reference: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.401-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NOS: 10444
                     FRA
APPLICANT: Gary L. Breton
TITLE OF INVENTION: WOLLEYC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES TITLE OF INVENTION: WOLLEYC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION WUMBER: 0S/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
EMENTE: 2000-04-04
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 GCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLP 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 FLV--TGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQ 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AHQEGKKKSPNNGV-----LFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 VVL---SVTLAATSISMLAPSGSVVYQRRIFGSE-LFSIID-KPTQLDPLDPSGKQP--E 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 IEKGELAFEKVSFRY-GGGETDVLRNISFHIRPGETVALAGATGSAKSSLVQLIPRLYDV 387
                                                                                                                                                                                                                                                                                                                                                                                                      51 VITAVGGKMILISIVGLIFSIANVYVSSHASIGFGTDLRTGLFGKIQQLSFFDIDRFSTA 110
                                                                                                                                                                                                                                                                                                                                                                   110 VLTYVSTAAITISAIRTTRRVFLE------CTLR-----QEVWHF--DKQSNG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 ---KDKSESLRDTVIHASNIIVSIFPVMQLVMNLSIIAILWMGGHKVMTGEL-KVGELIS
                                                                                                                                                                                                                                                                                7.3%; Score 468; DB 5; Length 574; 27.7%; Pred. No. 9e-29; Live 110; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                        11 Similarity 27.7%; Proceedings; Proceedings; Conservative 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 SEMYREIYYSQQI 572
                                                                                                                                                                                                     ; ORGANISM: B.fragills
US-09-540-2098-6190
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Best Local S:
Matches 153
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                                                                                                                                                                                            288 CIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSV---VYQRRI 344
                                                                                                                                                                                                                                                                                          513 ETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEAL--NRVSK 570
                                                                                                         72; Gaps
                                                                                                                                                                             232 ----RAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYF 287
                                                                                                                                                                                                                                           132 IFTTALTAMMYMACNGVMQGSLF-VGDLVLINQLVFQLSVPLNFL---GSVYRDLKQSLI 187
                                                                                                                                                                                                                                                                           345 FGSELF -----SIIDKPTQLD ----PLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQ 392
                                                                                                                                                                                                                                                                                                                       393 VLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSSGRILLDGLELGQYNVKWLRS 452
                                                                                                                                                                                                                                                                                                                                                                     453 RIRLYQQEPVLFRGTIFONIANGFMDEQRDLPREKQMELVQKACKASNGDVFINELPNGY 512
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.7%; Score 434; DB 6; Length 475; Best Local Similarity 28.6%; Pred. No. 2.9e-26; Matches 131; Conservative 79; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 4
; LENGTH: 475
; TYPE: PRT
• ORGANISM: Asbya gossypii
US-10-076-157-4
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Search completed: April 27, 2002, 07:58:51 Job time: 752 sec

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APPLICANT: Duvick, Jon
TTLE OF INVERFUN: Compositions and Methods for Funmonisin Detoxification
FILE REPERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224
CURRENT APPLICATION NUMBER: US/09/351,224
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID MOS: 11
SEQ ID NO 11
LENGTH: 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MADESEKPRPNODGSESSSHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSG
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Query Match 100.0%; Score 6453; Best Local Similarity 100.0%; Pred. No. 0; Matches 1263; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09351224 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: p-glycoprotein US-09-351-224-11
     TYPE: PRT
ORGANISM: Exophiala spinifera
 1280
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    /cgn2_6/ptodata/2/ppaa/USO6_COMB.pep:*
    /cgn2_6/ptodata/2/ppaa/USO8_COMB.pep:*
    /cgn2_6/ptodata/2/ppaa/USO9_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-351-224E-11
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ORGANISM: Exophiala spinifera
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LOCATION: 157
OTHER INFORMATION: Xaa
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APPLICANT: BUNICK, JOD
APPLICANT: G1111am, Jacob
APPLICANT: G111am, Jacob
APPLICANT: G111am, Jacob
APPLICANT: Grasta, Otto
APPLICANT: Crasta, Otto
TITLE OF INVENTION: Composition and Methods
TITLE REFERENCE: 5718-11
CURRENT APPLICATION NUMBER: US/09/351,224E
CURRENT FILIAG DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11263 Query Match 100.0%; Score 6453; Best Local Similarity 100.0%; Pred. No. 0; Matches 1263; Conservative 0; Mismatches and Methods - Any Amino Acid ; Sequence 11, Application US/09351224E; GENERAL INFORMATION:

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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
; OTHER INFORMATION: p-glycoprotein US-09-351-823-11
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GENERAL INFORMATION:
APPLICANT: Duviok, Jon
TITLE OF INVENTION: Compositions and Methods for Fundmonisin Detoxification
FILE REFERENCE: 5718-56
CURRENT APPLICATION NUMBER: US/09/351,823
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
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ORGANISM: Exophiala spinifera
FEATURE:
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GENERAL INFORMATION:
APPLICANT DUVICK, JON
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/677,488
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR APPLICATION NUMBER: 09/351,224
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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100.0%; Score 6453;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches
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ORGANISM: Exophiala spinifera
                                                                                                                                          DQA 1263
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LENGTH: 1263
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                                   RDLPREKOMELVOKACKASNGDVF1NELPNGYETEVGERAGALSGGQRQR1A1ARS11SD
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US-09-677-488A-11
Sequence 11, Application US/09677488A
GENERAL INFORMATION:
APPLICANT: Maddox, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
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APPLICANT: DUVICK, Jon
TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification
FILE REFERENCE: 35718/204101 (5718-111B )
CORRENT APPLICATION NUMBER: 05/09/677,682
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR PILING DATE: 1999-07-12
                                                                                                                                                                                                                                                961 SSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIRETEENKKKGPVGGCPVD 1020
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ORGANISM: Exophiala spinifera
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SOFTWARE: PatentIn Ve
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APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fum; TITLE OF INVENTION: Detexification
FILE REFRENCE: 35718/204100
FURENT APPLICATION NUMBER: US/09/677,488A
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR APPLICATION NUMBER: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1263
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US-09-677-488A-11
                                                                                                                                                                               TYPE: PRT
ORGANISM: Exophiala spinifera
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LOCATION: 157
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US-09-677-682A-11
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Sequence 11, Application US/09677682A

GENERAL INFORMATION:
APPLICANT: DUVICK, Jonn
APPLICANT: Gilliam, Jacob
APPLICANT: Colkeris, Otto
TITLE OF INVENTION: Compositions and Methods for Fumonisin
FILE REFERENCE: 3718/204101
CURRENT APPLICATION NUMBER: US/09/677,682A

CURRENT FILING DATE: 1990-07-12

NUMBER OF SEQ ID NOS: 11

SEQ ID NO: 11

SEQ ID NO: 11

SEQ ID NO: 11

SEQ ID NO: 11 Indels ö 100.0%; Score 6453; Similarity 100.0%; Pred. No. 0; 53; Conservative 0; Mismatches NAME/KEY: VARIANT
LOCATION: 157
COTHER INFORMATION: Xaa - Any Amino Acid
US-09-677-682A-11

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CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SEGVIPMARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1263
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                                                           TYPE: PRT
ORGANISM: Exophiala
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; OTHER INFORMATION:
US-09-677-682B-11
                                                                             FEATURE:
NAME/KEY: VARIANT
LOCATION: 157
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GENERAL INFORMATION:
APPLICANT: DUVICK, JON
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Detoxification
FITLE REFERENCE: 35718/204101
GURRENT APPLICATION NUMBER: US/09/677,682B
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100.0%; Score 6453; DB 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09882694
GENERAL INFORMATION:
APPLICANT: Maddox, Joyce
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Compositionis and Methods for TITLE OF INVENTION: Obecoxification
FILE REFERENCE: 3578,220825
CURRENT FALLING DATE: 2001-06-12
PRIOR PPLICATION NUMBER: 09/951,224
PRIOR PPLICATION NUMBER: 09/951,224
PRIOR PPLICATION NUMBER: 09/351,224
PRIOR PPLICATION OF 11
SEGO ID NO: 11
SEGO ID NO: 11
ENGTH: 1263
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LOCATION: 157
COTHER INFORMATION: Xaa - Any Amino Acid
US-09-882-694-11
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9. Car-U-0598-27499-2

9. Car-U-0598-27499-2

9. GENERAL INFORMATION:

9. APPLICANT: Startud, Paul L.

APPLICANT: General, Maarten

1 TILE OF INVENTION: Multiple Drug Resistance Gene atrC of TITLE OF INVENTION: Matten

1 TITLE OF INVENTION: Aspergillus Midulans

9. NUMBER OF SEQUENCES: 3

1 CORRESPONDENCE 11 Lilly and Company

ADDRESSEE: Eli Lilly and Company

5. TREET: Lilly Corporate Center
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APPLICANT: BUVICK, Jon
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Crasta, Oswald K.
TITLE OF INVENTION: Compositions and Methods f
TITLE OF INVENTION: Compositions and Methods f
TITLE OF INVENTION: Compositions and Methods f
TITLE OF INVENTION: Composition
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/882,694A
CURRENT FILING DATE: 1099-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
LEMCHT: 1263
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100.0%; Pred. No. 0;
iive 0; Mismatches
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US-09-882-694A-11
                                                                                                                                                         Sequence 11, Application US/09882694A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Exophiala spinifera
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Matches 1263; Conservative
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NAME/KEY: VARIANT
LOCATION: 157
                                                                               DQA 1263
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US-08-612-734-2
Sequence 2, Application US/08612734
Sequence 2, Application US/08612734
GENERAL INFORMATION:
APPLICANT: Peery, Robert B
APPLICANT: Tobin, Matthew B
TITLE OF INVENTION: MULTPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: MULTPLE DRUG RESISTANCE
TITLE OF INVENTION: MULTPLE DRUG RESISTANCE
TITLE OF INVENTION: MULTPLE DRUG RESISTANCE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q.
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/612,734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGDVFINELPNGYETEVGERAGALSGGQRQRIAJARSIISDPKILLLDEATSALDPKAEK 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1308;
                                                                                                  ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.2%; Score 2270; DB 1; Best Local Similarity 39.8%; Pred. No. 2.5e-208; Matches 512; Conservative 225; Mismatches 438;
                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
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CLASSIFICATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFRENCE/DOCKET NUMBER: X-117
TELECOMMUNICATION INPORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein PCT-US98-27499-2
Indianapolis
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                                                                                                                                                                                                             983 TKARSAANYILMLRTLKPTIR-ETEENKKKGPVGGCPVDLEDIEFRYRQRDSARVLRGVS 1041
                                                                                                                                                                                                                                                                                                                                                                                  MTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQ 1101
                                                                                                                        QC-STTSLWMETGPGGCVWCTSTPAFGWLPQNSSRD------EARS--RKLGKL 873
                                                                                                                                                                                                                                                      932 MEFLAIALGFCIAVDNWLQVSTTQLN-----FISSSWAFCLPVQAAAQYLAYSTSF 982
                                                             DIELLDIPEQISGALTSQLSALPTQLQEL------ISANFLIYIVVGQHRLE 828
                                                                                                                                                         929 VCISVVPILLACG-----FLRFYMLAQFQQRSKSAYEGSASYACEATSAIRTVASL 979
LSG---HAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQ
                         LPESMFHKLRHDANFWSLMFFVVGTAQFISLSINGTAFAICSERLIRRARSQAFRSILRQ
                                                                                        DISFEDREENSTGALTSFLSTETKNLSGVSGVTLGTIIMTSTTLGAAMIIALAIGWKLAL
                                                                                                                                                                                         974 CRK -- CWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQS
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APPLICANT: de Waard, Maarten A.
APPLICANT: Peery, Robert B.
APPLICANT: Peery, Robert B.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
CORRESPONDENCE: 3
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/27300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WEBSTER, Thomas D.
REGISTRATION NUMBER: 39,872
REFERRNCE,/DOCKET NUMBER: X-11766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9827300 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORRESEE: Ell L. ADDRESEE: Ell L. STREET: Lilly Corpor CITY: Indianapolis STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASOWKLALITMSVIPAIFLVT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 KKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISML 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 APSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 RIRLVQQEPVLFRGTIFQNIANG-----FMDEQRDLPREKQMELVQKACKASNGDVFINE 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 LPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLIDEATSALDPKAEKVVQEALNR 567
                                                                                                                                                                                                                                                                                                                                                                                                                           SFFTLYRYASRKDILIILVSAICAIAAGAALPLFTILFGSLASAFQGISLGTMPYHEFYH 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVDHFVLWFVYLFIGKFVLTYVSTAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNG 152
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                       35 DNEKPHDHHSLSDTIMAPPDGKKKDHGKAVDLNDDSLFAHLQEHEKEVLKRQLDAPSVKV 94
                                                                                                                                                                                                                                                                                                                                                                                                        34 -YLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYNSGDGSPEAFKA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 VSKDRTTLVIAHKLATVKSAGNIAVISQCKIVEQGTHHELIEFGCHYAALVRAQ-----
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630 AAEGRITIVIAHRLSTIKTAHNIVAMVGGKIAEQGTHDELVDRKGTYKKLVEAQRINEEK
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                                                                                                                                                                                                                                                                                                          Indels 172;
                                                                                                                                                                                                                                                                            Length 1349;
                                                                                                                                                                                                                                                                        Query Match 30.3%; Score 1956; DB 10; Best Local Similarity 35.8%; Pred. No. 5.9e-178; Matches 491; Conservative 229; Mismatches 478;
                                                                                                                                                                                                                                                                                                                                           4 ESEKPRPNQDGSESSSHPPP-EKETEGSISD-------
                                                                  X-9681
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Any E
REGISTRATION NUMBER: 33,894
REFERENCE/DOCKET NUMBER: X-968
REFERENCE/DOCKET NUMBER: X-968
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGHH: 1349 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                         ; MOLECULE TYPE; protein US-08-612-734-2
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llarity 36.0%; Pred. No. 2e-175;
Conservative 231; Mismatches 483; Indels 128; Gaps
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                                                                                                                                                                                                                                                              DILIMVISTICATAAASTEGRIMLYQISY------DEFYDELTRNVLYEVYL 158
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                       TELEFAX: 317-276-2763
: INPORMATION FOR SED ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1334 amino acids: TYPE: amino acids: TYPE: amino acids: MOLECOLE TYPE: protein pcr-US98-27300-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-2763
                                                                                                                                            Query Match
Best Local Similarity
Matches 490; Conserv
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-----FISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIRE-TEENKK 1010
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                                                                                                                                                                                                                                                                                                                                                                               YDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLAL-EAELSEE-LC 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1189 ALDTQSERLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLR 1248
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                                                                                                                 ---FYRFYMLAOFOSRS-----KLAYEGSANFACEATS---SIRTVASLTRERDVWEIYH 975
                                                                                                                                                                907 VE---QG---LAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLN--- 957
| : | ; ; | ; ; | STETKHLSGVSGVTLGTILMTSTTLGAAIIIALAIGWKLALVCISVVPVLLACG
                                                                     847 CTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGH
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GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF TITLE OF INVENTION: MULTIPLE OF INVENTION: ASPERGILIUS FLAVUS
CORRESPONDENCE ADDRESS:
ADDRESSE: BIL Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 46285

ZIP: 46285

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/395,246A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas 6.
REGISTRATION NUMBER: 35784
REFERENCE/DOCKET NUMBER: x968
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-459
TELEFAX: 317-277-1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1307 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1319 GRYYELVNLOSL 1330
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GDLGALLENNTNSSNITDTVPVMNLEEDWTRYAYYYSGIGAGVVAAYIQVSFWCLAAGR 145
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    -----FNNYNSG---DGSPEA-FKADVDHFVLWFVYLFIGKFVLTYVSTAAITISAIR 125
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                                                                                                                                                                                                              PTLYQGSVRENVTLALEAE - - LSEELCQGRLPARPMLWILSSLYQKALKRLAAQRGMQFS
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                                           IALGFCIAVDNWL------QVSTTQLNFISSSWAFCLPVQAAAQYLAYSTSFTKARSA
                                                                    MALGF -----WYGGSLLGHGEYSLFQFYVCFSEVIF --GAQAAGTVFSHAPDMGKAKHA
                                                                                                 ANY ILWLRTLKPTIRE - - TEENKKKG - PVGGCP - - VDLEDIEFRYRQRDSARVLRGVSMT
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GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: STECKER, PENNY J.
APPLICANT: STECKER, PENNY T.
APPLICANT: CREENELS L.
TITLE CANT. CREENEY, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,911
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09: 18
NUMBER OF ESO ID NOS: 18
SOFTWARE: FastSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                           1222 RNVDVIFVFANGRIAETGTHAELQRLRGRYYEMCLAQSLD 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Macaca fascicularis
US-09-672-810-4
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-672-810-4
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Best Local Si
Matches 428;
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SEQ ID NO 4
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                                                                                                                                                                                                                           117 AAITISAIRTTRTLRNFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFT 176
                                                                                                                                                                                                                                            VQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVL 236
                                                                                                                                                                                                                                                                                                    FWKGFRMYQNGEVADV--GKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIID 354
                                                                                                                                                                                                                                                                                                                                                                                                                   KPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428
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                                                                                                                                        10 KPLPKSPGTGSTTTGHSVSHAEEVLDRQLHTPVSQIGFFGIYRYATRWDVAILFGSALAA 69
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| IAGGAALPLFTVLFGRLTSTFQDIATHRITYDHFHHELTKNVVYFIYLGAAEFVAIYLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALA
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                                                                                    Indels 172;
                                                         Length 1307;
                                                      Score 1780; DB 7;
Pred. No. 5.6e-161;
2; Mismatches 500;
                                                                                    Conservative 222;
                                                      27.68;
   protein
                                                                      Similarity
; MOLECULE TYPE:
US-08-395-246A-2
                                                      Query Match
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ð	306	3 36
qq	326	SKEYS-IGQVLTVFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKS 384
çy op	366	GKQPEGCLGGIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLE 425   : :
ý 5	426	œ
2		,
Oy Dp	486 498	EKOMELVOKACKASNGDVETNELPRGYETEVGERGALSGOGORGILATARSIISDFRILL 545
φ	546	LDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHH 605
qq	557	LDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAGFDDGVIVEKGNHD 616
οy	909	ELIEFGCHYAALVRAQDLGADEQQEHEKTLHEKAAREAAGERPALE-RTHTTATSQAGDL 664
QΩ	617	ELMKEKGIYFKLVTMQTAGNEIELENAADESKSEIDTLEMSSHDSGSSLIRKR 669
ģ i	599	YEOKNLYW-CFLLSTITV
QQ O	670	STRRSVRGSQCQDRKLSTKEALDESIPPVSFWRIMKLNLTEWPYFVVGVFCA 721
Qy Gb	704	LICAATFPGGALLFSRLLTVFELSGHAAQERADFYILMFVVALGNLVGYFTIGWTCN 761 :
φ	762	VISQYVTHRYQAAMFORVLDQDIELLDIPEQISGALTSQLSALPTQLQELISANFLIYIV 821
qq	782	<pre>:::    : :  : :    :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :   :     :   :   :   :   :   :     :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :</pre>
οy	822	VGQHRLEQCSTTSLMMETGPGGCVWCTSTPAFGW
QQ	839	ITONIANLGTGIIISLIYGWQLTLLLAIVPIIAIAGVVEMKMLSG 884
Οy	859	NSSRDEARSRKLGKLCRKCWACKRSSTRDPDRLIFDSRRPCSPTVLGHV-EQGLA 912
qq	885	GALKDKKELEGAGKIATEAIENFRTVVSLTGEGKFEHMYDGSLQVPYRN 933
ôy	913	KIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLNFISSSWAFCLFV 969
qq	934	SLRKAHIFGITESFTOAMMYFSYAGCFFFGAYL-VAHSLMSFEDVLLVFSAVVFGA 988
δ	970	OAAAQYLAYSTSFTKARSAANYILMLRTLKPTIRE-TEENKKKGFVGGCPVDLEDIEFRY 1028
QQ	989	DYAKAKVSAA
0y	1029	RQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGRISFAHENIAEM 1088
Q	1048	PTRLDIPVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERFYDPLAGKVLLDGKEIKQL 1107
οy	1089	MSLVQQEPTLYQGSVRENVTLALEAELSEE
QΩ	1108	NOQWLRAHIGIUSQEPILFDCSISENIAYGDNSRVVSQEEIVRAAKEANIHAFI-ESLPN 1166
οy	1147	KALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDBATSALDTQSERLVQAALDEAS 1206
qq	1167	
Οy	1207	TSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRIRGRYYEMCLAQS 1259
QQ	1226	EGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSMVSVQA 1278

Search completed: April 27, 2002, 07:55:43 Job time: 604 sec

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6455
1 MADESEKPRPNQDGSESSSH......LQRLRGRYYEMCLAQSLDQA 1263
                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-352-552-2
US-08-612-758-2
US-08-996-545-2
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US-08-320-2
US-08-352-4
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US-08-583-2
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US-09-120-513-2
US-09-120-513-2
US-09-450-105-2
US-08-461-384-8
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Maximum Match 100%
Listing first 45 summaries
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                          Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
(15-08-966-644-2
) Sequence 2, Application US/08996644
) Patent No. 5945324
) GENERAL INFORMATION:
) APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten
TITLE OF INVENTION: Multiple Drug Resistance Gene atrC of
TITLE OF SEQUENCES: 3
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,644
                       US-08-460-907B-4
US-08-461-179A-4
US-08-726-320-4
US-08-726-320-4
US-08-716-4
US-08-141-89-2
US-08-463-092B-2
US-08-463-092B-2
US-08-463-109A-2
US-08-463-109A-2
US-08-463-109A-2
US-08-463-109A-2
US-08-463-109A-2
US-08-463-092B-7
US-08-463-092B-7
US-08-463-092B-7
US-08-463-092B-7
US-08-463-092B-7
US-08-463-092B-7
US-08-09-061-764A-19
US-09-061-764A-19
US-09-061-764A-19
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ADDRESSEE: Eli Lilly and Company STRET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x-11765
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REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEFAX: 317-276-2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: I.ENGTH: 1308 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-644-2
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| ALGFWYGCRLVSLGETSMYSFFVAFLSVFFAGQASAQLFOWSTSITKGINATNYIAWLHO 1042
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           LSCHAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIE 785
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                                                                                                                 DVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVL 320
                                                                                                                                                       SVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQN 380
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                                      QEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALI
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APPLICANT: GA Waard, Paul L.
APPLICANT: GA Waard, Maarten
TITLE OF INVENTION: Multiple Drug Resistance Gene atrC of
TITLE OF INVENTION: Aspergillus Nidulans
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,552
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REGISTATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-117
TELECOMMUNICATION INFORMATION:
TELEFAX: 317-276-334
TELEFAX: 317-276-376
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09352552 Patent No. 6060264 GENERAL INFORMATION:
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                                                                                                                                                                   APPLICANT: Beery, Robert B.
APPLICANT: Statrud, Paul L.
APPLICANT: Statrud, Paul L.
APPLICANT: Tobin, Matthew B.
TITLE OF INVENTION: Multiple Drug Resistance Gene of
TITLE OF INVENTION: Aspergillus Fumigatus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Eli Lilly and Company
STREET: Lilly Corporate Center, DC1501
CITY: Indianapolis
STATE: Indiana
COUNTR: U.S.A.
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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llarity 35.8%; Pred. No. 2e-195;
Conservative 229; Mismatches 478;
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APPLICATION NUMBER: US/08/612,734B
FILING DATE: 08-MAR-1996
                                        Sequence 2, Application US/08612734B Patent No. 5914246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Craig, Anne I.
REGISTRATION NUMBER: 32,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-354-9570
TELEPAX: 617-354-4043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatit
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1349 amino acids
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Best Local Similarity
Matches 491; Conserv
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
US-08-612-734B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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APPLICANT: Statrud, Paul L.
APPLICANT: de Waard, Maarten A.
APPLICANT: de Waard, Maarten A.
APPLICANT: Peerly, RObert B.
APPLICANT: Peerly, RObert B.
TILE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
TORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company

Sequence 2, Application US/08996545 Patent No. 5928898

Patent No. 5928898 GENERAL INFORMATION:

ADDRESSEE: Ell Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,545

FILING DATE

ZIP: 46285 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of

U.S.

COUNTRY:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEDSERFY, 39,872
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11766
TELEPHONE: 317-276-334
TELEFAX: 317-276-334
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1334 amino acids

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980 TREQDVWGVYHDQLQKQGR-----Y850 TOLLSVLRSSLL----YASSQA 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1068 GKAKNAAAQFKKLFDSKPTIDIWSDEGEKLESMEG-EIEFRDVHFRYPTRPEQPVLRGLN 1126
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                                                                                LSG----HAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQ 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               929 VCISVVPILLACG------FLRFYMLAQFQQRSKSAYEGSASYACEATSAIRTVASL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEFLAIALGFCIAVDNWLQVSTTQLN-----FISSSWAFCLPVQAAAQYLAYSTSF 982
                                                                                                                                                                                                                                                                                                                                                                             RKVPVGTLGYSLLKCI-LIMFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFE 725
                                                                                                                                                                                                                                                                                                                                                                                                      750 KKVPEQFEKYSLWTLVKFIGAFNRPELGYMLIGLTFSFL-AGGGOPTOAFLYAKAISTLS 808
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335 KQQVILGMMIGGMFGIMFSNYGLGFWMGSRFVVGKEV-NVGQVLTVLMSILIGSFSLGNV 393
                                                                                                                                           RIRLVQQEPVLFRGTIFQNIANG-----FMDEQRDLPREKQMELVQKACKASNGDVFINE 507
                                                                                                                                                                                                                                                                                                                                      333 APSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQ
                                             874 CRK--CWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQS
                                                                                                                                                                                                                                                              568 VSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGSELFSIIDKPTOLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAG 404
                                                                                                                                                                                                                                                    DWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYNSGDGSPEAFKADVDHFVLWFVYL 104
                                                                                                                                                                                                                                                                                                                  105 FIGKFYLTYVSTAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNR 164
                                                                                                                                                          Gaps
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                                                                                                                                                         Indels 128;
                                                                                                                           Length 1334;
                                                                                                                         Query Match 30.1%; Score 1940; DB 2; Best Local Similarity 36.8%; Pred. No. 9.5e-194; Matches 490; Conservative 231; Mismatches 483;
LENGTH: 1334 amino acids
TYPE: amino acid
TOPOLOGY: Inhear
MOLECULE TYPE: protein
US-08-996-545-2
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RESULT 4 US-08-996-545-2

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                                                                                                                                                                                                                                                                                                                                                  SALPTQLQEL ------ISANFLIYIVVGQHRLEQC-STTSLWMETGPGGCVW 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VE---QG----LAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLN--- 957
            741
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                                                                                                                                                                                                                CTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIRE-TEENKK
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                                                RGTIFONIANGFMDEQRDLPRE-KOMELVQKACKASNGDVFINELPNGYETEVGERAGAL
                                                                                                 SGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLAT
                                                                                                                                                VKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHE------
                                                                                                                                                                                               -----KTLHEKAAREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCI-LI
                                                                                                                                                                                                                                                 MFYEOKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFEL --- SCHAAQERADFYILM
                                                                                                                                                                                                                                                                          754 ASFNRPEIPY-MLIGLVFSVLAGGGQPTQAVLYAKAISTLSLPESQYSKLRHDADFWSLM
                                                                                                                                                                                                                                                                                                  FFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQL
                                                                                                                                                                                                                                                                                                                           813 FFVVGIIOFITQSTNGAAFAVCSERLIRRARSTAPRTILRQDIAFFDKEENSTGALTSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09328320
Patent No. 6228615
GENERAL INFORMATION
APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
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APPLICANT: Peery, Robert B.

APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD (TITLE OF INVENTION: Aspergillus Nidulans NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESS: Lilly and Company STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%; Score 1940; DB 4; ilarity 36.8%; Pred. No. 9.5e-194; Conservative 231; Mismatches 483;
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,320
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1334 amino acids TYPE: amino acid amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-328-320-2
                                                                                                                        ADDRESSEE: Eli Lilli
STREET: Lilly Corpo:
CITY: Indianapolis
STATE: Indiana
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Best Local Similarity
Matches 490; Conserv
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                                                              CTITKNIRHGLIGTKYENESEDKVRELIENAAKMANAHDFITALPEGYETNVGQRGFLL
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                                                                                              SGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLAT
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APPLICANT: Peery, Robert B
APPLICANT: SKATING, Paul L
APPLICANT: Thornewell, Susan J
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
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US-008-612-521-2
Sequence 2, Application US/08612521
Parent No. 5786463
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TITLE OF INVENTION: CRYPTOCOCCUS NEOFORMANS NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,521
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy
REGISTRATION NUMBER: 33,894
                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                           ZIP: 46285
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMUNICATION INFORMATION:
TELEPHONE: 317-276-3169
TELEFAX: 317-276-3169
TELEFAX: 317-276-3169
TELEFAX: SEQUENCE OF S
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Patent No. 5773214
GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: SKATUAU, Paul L.
TITLE OF INVENTION: MULTIPLE OF UNDERTON: ASPERGILLUS FLAVUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1307;
                                                                ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PREADENT RELEASE #1.0, VERSION #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,246C
                                                                                                                                                                                                                                                                                                                                                                                                                       27.6%; Score 1780; DB 1; ilarity 34.3%; Pred. No. 6.1e-177; Conservative 222; Mismatches 500;
ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                     CLASSIFICATION: 435
ATTORREY/AGENY INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35784
REFERENCE/DOCKET NUMBER: x968
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1307 amino acids
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
WOLECULE TYPE: protein
US-08-395-246C-2
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QY         545 A           QY         592 V           Db         605 V           QY         652 R           QY         652 R           QY         656 P           QY         686 F           QY         686 F           QY         732 Q           DD         775 R           QY         732 Q           DD         775 R           QY         732 Q           QY         887 D           DD         989 A           QY         1044 P           QY         1145 P           QY         1145 P           QY         1145 P           QY         1145 P           QY         1203 G           QY         1203 G           QY         1263 Q           QY         1263 Q	. AIARAIIKDPKILLLDEATSALDTKSEKLVQAALDKASKGRTTIVIAHRLSTIQKAYNII 604	: VISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHEKTLHEKAAREAAGERPALE 651   i::  :	RTHTTATSQAGDLEKRKVPVGTLGYS-LLKCILIM 68	PKHNPMTFFFDKDYPGDDESD1YS1LSDDASDIGLHTGEKQR-PVSRMSLSHLMQPVKEE 7	AYSEWTLE		RHDANFWCLMFLMIGIVSLVLXSVQGTLFAXSSERWYRARSQAFRVLHQDISFFDQQE 834		NTTGALTATLSAGTKELTGISGVTLGTILIVSVNLVASLGVA	EQCSTTSLWMETGPGGCVWCTSTPAFGWLPQNSSRDEARSRKLGKLCRRCWACK-RSSYR 886	DPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLA 93	::     :	IALGECIAVDNWLQVSTTQLNFISSWAFCLPVQAAAQYLAYSFTKARSA 988	MALIGE" -	ANYILWIRTLKPTIRETEENKKKG-PVGGCPVDLEDIEFRYRQRDSARVLKGVSWT 1043 			PTLYQGSVRENVTLALEAELSEELCQGRLPARPMLWILSSLYQKALKRLAAQRGMQFS 1161		GGGRQKLATARALIKHVELLLDEATSALDTOSERLVQAALDEATSKTTAVAHRLSTI 1221    :	RNVDVIFVFANGRIAETGTHAELQRL		T 8  52-4  APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman, ael M. TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA FUTURE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA ENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS CUNRENT APPLICATION DATA: CUNRENT APPLICATION DATA: CUNRENT APPLICATION DATA: APPLICATION NUMBER: 092,575 FILING DATE: 24-SEP-1990 APPLICATION NUMBER: 892,575 APPLICATION NUMBER: 892,575 APPLICATION NUMBER: 845,610 FILING DATE: 28-MAR-1986 ILING DATE: 28-MAR-1986 ILING DATE: 1280
Db 65  Qy 59  Qy 68  Qy 68  Qy 68  Qy 73  Qy 82  Qy 82  Qy 82  Qy 93  Qy 116  Qy 116  Qy 116  Qy 116  Cy 122  Cy 126  Cy 126  Cy 126  Cy 116   ın.												-										~ 'S 1 2 % E S 5 1 % 5 1 5 1 5 1 5 1	
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                                                               Gaps
                                                                                     24 EKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNN---- 79
                                                                                                     309 VADVGKVETVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQ
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                                   Query Match 25.4%; Score 1640.5; DB 6; Length 1280; Best Local Similarity 32.3%; Pred. No. 2.7e-162; Matches 427; Conservative 243; Mismatches 491; Indels 163;
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                                                                               -----GLMPNTLEGN 1034
                                1035 VFFGEVVENYPTRPDIPVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERFYDPLAGKY 1094
                                                                  SFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLALEAEL--SEELCQGRLPARP 1136
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GENERAL INFORMATION:
APPLICANT: SIACL, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCORROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Mealo Park
STAFE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FGAMAVGQVSSFAPDYAKAKISAAHIIMIIEKTPLIDSYSTE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
RECISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08784649A
Patent No. 5830697
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SEQUENCE CHARACTERISTICS:
LENGTH: 1279 amino acids
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US-08-784-649A-2
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                                                                                             86 EDLMSNITNRSDINDTGFFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIH 145
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APPLICANT: Roninson, 190r B
AITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligeal Agents Specific for P-glycoprotein
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                                                                                                                    1211 KVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSMV 1270
1078 ISFAHENIAEMSPRIZYGHMSLVQQEPTLYQGSVRENVTLALEAEL--SEELCQGRLPAR 1135
1093 VLLDGKEIKRLNVQWLRALIGYSQEPTLFDCSIAEMIAYGDNSRVVSQEETVRAKEAN 1152
                                                                   RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMC 1255
                                                    1136 PMLWILSSLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSE 1195
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%; Score 1629.5; DB 2; 32.0%; Pred. No. 3.9e-161; iive 242; Mismatches 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 594086nan, Kevin E
REGISTRATION NUMBER: 35,303
REFRENCE/POCKET NUMBER: 95,1121
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
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15-NOV-1996
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        Sequence 2, Application US/08752447 Patent No. 5994088 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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tes 424; Conservative
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TOPOLOGY: linear
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CITY: Chicago
STATE: Illinois
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  1196 RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMC 1255
                            84 ILPSVINQSEINSTQIVSDSSLEEDMAMYAYYYTGIGAGVLIVAYIQVSLWCLAAGRQIH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYNUCLEOTIDE AND POLYPEPTIDE
SEQUENCES ENCODING RAT MDRIB2 AND
SCREENING METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.8%; Score 1601; DB 3; :ilarity 32.6%; Pred. No. 3.9e-158; Conservative 247; Mismatches 504;
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APPLICATION NUMBER: US/09/120,513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKine Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/09120513; Patent No. 6025160
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Brun, Kimberly
APPLICANT: Chenery, Richard
APPLICANT: Ellens, Harma
APPLICANT: Field, John
APPLICANT: Yue, Lin
TITLE OF INVENTION: SEQUENCES
CORRESSOURCES: 2
CORRESSOURCES: 4
CO
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REFERENCE/DOCKET NUMBER: GP:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5015
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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NAME: King, William T
REGISTRATION NUMBER: 30,5
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COMPUTER READABLE FORM:
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STRANDEDNESS: sin
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CLASSIFICATION:
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                                                                                                 1256 LAQS 1259
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Best Local Si
Matches 425
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978 YSTSFTKARSAANYILWLRTLKPTI--RETEENKKKGPVGGCPVDLEDIEFRYRQRDSAR 1035
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                                                                                                                                                    PEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWY 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLEKR-----KVPVGTLGYSLLKCILIMFYEQKNL---YWCFL-LSTITVLICAAT 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 710 FPGGALLFSRLLTVFEL-SGHAAQER-ADFYILMFFVVALGNLVGYFTIGWTCNVISQVV 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               814 ANFLIYIVVGQHRLEQCSTTSLWMETGP----GGCVWCTSTPAFGWLPQNSSRDEARSRK 869
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                                                AFY AQKKMVEKY DVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAA IALAFWKGFRMYQNGE
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YSTSFTKARSAANYILMLRTLKPTI -- RETEENKKKGPVGGCPVDLEDIEFRYRQRDSAR 1035
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                                                                                                                                                                                                                                                                        THRYGAAMFQRVLDQDIELLDIPEQISGALTSQLS------ALPTQLQELIS 813
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                                                                                                                                                                                                                                                                                                                                                                                           842 TGIILSLVYG------WOLTLLLVVIIPLIVLGGII-----EMKLLSGQALKDKKELEI 889
                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQ-----SFWF 920
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                                                                                                                                                   674 DOERRISSKEDVDEDVP------MVSFWQILKLNISEWPYLVVGVLCAVINGCI 721
                                                                                                                                                                                            710 FPGQALLFSRLLTVFEL-SGHAAQER-ADFYILMFFVVALGNLVGYFTIGWTCNVISQVV 767
                                    608 IEFGCHYAALVRAQDLGADEQEHE--KTLHEKAAREAAGER---PALERTHTTATSQAG
54 EATSALDTESEAVVQAALDKAREGRTTIVIAHRLSTVRNADVIAGFDGGVIVEQGNHEEL
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APPLICANT: SKatrud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: AUREOBASIDIUM PULLULANS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell LIIIy and Company
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
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STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
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US-08-232-537-2
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kimberly Anne Brun
APPLICANT: Kimberly Anne Brun
APPLICANT: Kimberly Anne Brun
APPLICANT: Albard Juames Chenery
APPLICANT: John Anthony Feild
APPLICANT: John Anthony Feild
APPLICANT: John Yue
TITLE OF INVENTION: FOLINUCLEOTIDE AND FOLIVPEPTIDE SEQUENCES
TITLE OF INVENTION: ENCODING RAT MDRIB2 AND SCREENING METHODS THEREOF
FILE REPERRICE: GF-50008-D1
CURRENT FILICATION NUMBER: US/09/450,105
CURRENT FILING DATE: 1999-11-29
ERALIER APPLICATION NUMBER: 09/120,513
EARLIER APLICATION OFFE:
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 YS-IGQVLTVFFSILLGTFSIGHLAPNIEAFANARGAAYEIFKIIDNEPSIDSFSTKGHK 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.8%; Score 1601; DB 4; Length 1275; Best Local Similarity 32.6%; Pred. No. 3.9e-158; Matches 425; Conservative 247; Mismatches 504; Indels 128;
                   1214 VAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMCLA 1257
                                                                                                                                    Sequence 2, Application US/09450105 Patent No. 6169166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-450-105-2
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                                                                                                                     09-450-105-2
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Pred. No. 2.3e-127;
i; Mismatches 549; Indels 119; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGFWKLLLRCLRL----AKSDSPIIALGLAASIVSGGIILGEAIVFGNLISVLNDLESPD 757
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                                                                                                                                                                                                                                                                                                                                                                              32 SDYLRIFRYA-DKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYNSGDGSPEAF 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 GOYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQRDLPREKQMELVQKACKASNGD
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                               ETLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X9212
TELEPHONE: 317-276-2459
TELEPHONE: 317-276-1917
INFORMATION FOR SEQ ID NO: 2:
SECUENCE CHARACTERISTICS:
LENGTH: 1302 amino acids
TYPE: amino acids
TYPE: amino acids
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,537
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 29.3%; Pre
Matches 379; Conservative 245;
                                                                                                                                                                                                                                                                                                                   20.3%;
                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-537-2
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Best Local (
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951 VSTTQLNFISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIRETEENK- 1009
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                                                                                                                             ----WCTSTPAFGWLPQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSP
                                                                                                                                                               859 HVVAWKIAVVLLAAVPVMITAGYVRLRVLALAESR----HRSAYNDAASIAAEACRGIRT
                                                                                                                                                                                                      902 TVLGHVEQGL----AKIIQSFWFGRCFG----FHLSQSMEFLAIALGFCIAVDNWLQ
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Patent No. 5705332
CENERAL INFORMATION:
APPLICANT: Seaturd, Faul L.
TILE OF INVENTION: Multiple Drug Registance Gene Of
TILE OF INVENTION: Multiple Drug Registance Gene Of
TILE OF INVENTION: Aspergillus Fumigatus
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company/Patent Division
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                      SVPSLMS-SLSSDAGQLACLSGVAIGTIFTVCVSI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,880B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant G., Thomas
REGISTRATION NUMBER: 35784
REFERENCE/DOCKET WUMBER: X-9682
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 776_2459
TELEPHONE: (317) 276-2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::| :| :| :| :| :| 332 LALLLPP------IGLGAFFYGRAIRNLSRQIQRNLGTLTKIAEERLGNVKTSQSFAG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 LGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSS 432
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                                                                                                                                                           Length 791;
                                                                                                                                                           Query Match 10.0%; Score 647.5; DB 1; Length 7 Best Local Similarity 31.5%; Pred. No. 2.8e-58; Matches 188; Conservative 107; Mismatches 231; Indels
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHRACTERISTICS:

LENGTH: 791 amino acids

; TYPE: amino acid

; TYPE: amino acid

; MOLECULE TYPE: protein

US-08-394-880B-2
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Search completed: April 27, 2002, 07:47:09 Job time: 6726 sec

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April 27, 2002, 07:45:35 ; Search time 104.96 Seconds (without alignments) 1336.568 Million cell updates/sec
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2. SIDSI_gcgdata_hold_geneseq_geneseqp_embl_AA1981_DAT:*

3. SIDSI_gcgdata_hold_geneseq_geneseqp_embl_AA1991_DAT:*

3. SIDSI_gcgdata_hold_geneseq_geneseqp_embl_AA1991_DAT:*

3. SIDSI_gcgdata_hold_geneseq_geneseqp_embl_AA1991_DAT:*

4. SIDSI_gcgdata_hold_geneseq_geneseqp_embl_AA1991_DAT:*

5. SIDSI_gcgdata_hold_geneseqg_embl_AA1999_DAT:*

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6455
1 MADESEKPRPNODGSESSSH......LQRLRGRYYEMCLAQSLDQA 1263
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Exophiala spinifer	P. chrysogenum ABC	A. nidulans atrC p	Multiple drug resi	Protein encoded by	P. chrysogenum ABC	Multiple drug resi	Aspergillus flavus	Cynomologous monke	Cynomologous monke	Human multidrug re
KIES				7	89	S	4	0	Z.		'n	Z.	4	Э
SUMMARIES			£	AAY7263	AAB62488	AAY2181	AAY1643	AAY0263	AAB62495	AAW6287	AAR9925	AAB8106	AAB8106	AAW44073
			OB OB	22	22	20	20	20	22	19	17	22	22	18
		Query	Length	1263	1248	1308	1349	1334	1333	1408	1307	1283	1280	1280
	œ	Query	Match	100.0	37.1	35.2	30.3	30.1	30.0	27.7	27.6	25.7	25.6	25.6
			Score	6453	2392	2270	1956	1940	1934.5	1789.5	1780	1656	1654.5	1649.5
		Result	No.		74	m	4	2	9	7	<b>6</b> 0	6	10	11

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The patent discloses novel polynucleotides encoding Exophiala spinifera fumonisin degradative or transport enzymes such as flavin monocxygenase, aldehyde dehydrogenase, permease and p-divoprotein. A fumonisin esterase enzyme with at least one fumonisin degradative enzyme is useful for detoxifying fumonisin or a structurally related mycotoxin present in harvested grain, on application to a plant or to harvested grain of uring processing, or to processed grain that is to be used as almal or knwan feed, or as a slage. Nucleotide fragments of the present invention are useful as probes and primers. They can be introduced into microorganisms that multiply on plants to deliver enzymes to potential target crops. The genes encoding the degrading enzymes are introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the pathogenicity of a fungus producing fumonisin. The genes of the pathogenicity of a fungus producing fumonisin. The genes of the pathogenicity of a fungus producing fumonisin. The genes of the convention are fermented in a bacterial host and the resulting bacterial is processed and used as a microbial spray. The nucleotide sequences can be used alone or in combination to engineer microbes or other corganisms to metabolise fumonisin and resist its toxic effects. The present procein sequence is p-lycoprotein, a fumonisin
                                                                                                          Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food
                                                                                                                                                                                                                                                  Claim 1c; Page 77-82; 90pp; English.
                         WPI; 2001-14/345/15.
N-PSDB; AAD02694, AAD02695
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1263 AA; Sequence

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                                                                 ASLPLMSIIFGSFINKFNNYNSGDGSPEAFKADVDHFVLWFVYLFIGKFVLTYVSTAAIT 120
                                                                           121 ISAIRTTRILRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQAL 180
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                   Gaps
                                 1 MADESEKPRPNQDGSESSSHPPPEKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSG 60
                                            RDLPREKOMELVOKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRIAIARSIISD
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100.0%; Score 6453;
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Matches 1263; Conservative
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                       LTVFELSGHAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVL
                                                                                                                        PKILLLDEATSALDPKAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVE
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    P. chrysogenum ABC transporter aal sequence.

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lactam compounds from a micro-organism that comprises enhancing ABC dadenosine triphosphate (ATP)-binding cassette) transporter activity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents the P. chrysogenum ABC transporter aal protein sequence.
                                                                                                                                                                                                                                                                                                                                                                     Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins -
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llarity 41.3%; Pred. No. 1.7e-214;
Conservative 205; Mismatches 417;
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Schuurs TA, Nieboer M, Westerlaken I;
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                                                                          99EP-0203687.
99EP-0203687.
99EP-0203688.
99EP-0203690.
99EP-0203691.
99EP-0203693.
                                03-NOV-2000; 2000WO-EP11489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a multiple drug resistance gene atrC of Aspergillus nddulans. Host cells transformed with vectors comprising the atrC gene are used for the recombinant expression of atrC polypeptide. The atrC polynucleotide is used to produce nucleic acid molecules which are useful in diagnostic assays for detection of atrC polynucleotides. The atrC polypeptide may be used to identify agents which inhibit multiple drug resistance. These agents may be useful for the treatment of fungal diseases. New antifungal compounds may also be identified using the gene disruption or gene replacement strains of Aspergillus nidulans. The present sequence represents atrC polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 tesgrrqtfvtmppswrllyfvylgiarlvlsytyntlltyaayrivrnirhaylkaals 182
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                                        Multiple drug resistance, atrC; Aspergillus nidulans; fungal disease; gene disruption.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New multiple drug resistance gene atrC
                                                                                                                                                                                                                                                                                                                                                                                     De Waard MA, Peery RB,
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(UYWA-) UNIV WAGENINGEN AGRIC.

    A. nidulans atrC polypeptide.

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                                                                                                       Aspergillus nidulans.
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1057 1102 1117 1176 NPKLLLLDEATSALDTQSERLVQAALDEAST--SRTTIAVAHRLSTIRNVDVIFVFANGR 1234 602 619 662 725 883 943 LSGHAAQERADFYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFORVLDQDIE 785 877 982 997 ELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQ-RDLPREKQMELVQKACKAS 499 520 AQDLGADEQQEHEKTLHEKAAREAAGERPA-LERTHTTAT------SQAGDLE **VVQEALNRVSKDRTTLVIAHKLATVKSAGNIAVISQCKIVEQCTHHELIEFGCHYAALVR** 663 ignlavn --- - asahdnvneegegedvallevtetavtryptsirgrmnsikdrddye 566 KRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFE 846 WCTSTPAFGWLPQ-----KLCRKC 890 -----vfggipplvgagmvrirvdsrldrqtakkygtassiaseavnairtvsslaiee WACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLAI gdavksvødeglesalraanawdfvsslpg-glytpagsggsglsgggrqrialaralir 500 NGDVFINELPNGYETEVGERAGALSGGORORIAIARSIISDPKILLLDEATSALDPKAEK 786 LLDIPEQISGALTSQLSALPTQLQELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGCV ALGFCIAVDNWLQVSTTQLNFISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRT LKPTIRETEENKKKGPVGGCPVDLEDIEFRYRQRDSARVLRGVSMTIEPGQFVAYVGASG A-LEABLSEELCOGRLPARPMLWILSSLYOKALKRLAAQRGMQFSGGQRQRIAIARALIR CGKSTLIALSERFYDPTSGRISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTL Multiple drug resistance protein of A. fumigatus. resistance protein; AfuMDRI; inhibition activity. 1235 IAETGTHAELQRLRGRYYEMCLAQSLD 1261 \$ AAY16434 standard; Protein; 1349 (first entry) drug

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980 treqdvwgvyhdqlqkqgr----yassqa 1016
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            eaealeadadmdaddfgqegvtriktavsssnsldavdekarlemkrtgtgksvssavls 749
                                                                                                                                                                                               RKVPVGTLGYSLLKCI-LIMFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLLTVFE 725
                                                                                                                                                                                                                                                                                     829 QC-STISLWMETGPGGCVWCISTPAFGWLPQNSSRD------EARS--RKLGKL 873
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                                                                                  LSG ---HAAQERADEYILMFFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      874 CRK--CWACKRSSYRDPDRLIFDSRRPCSPTVLGHVEQGLAKTIQSFWFGRCFGFHLSQS
LPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEALNR
                                                                                                                               -----DLGADEQQEHEKTLHEKA----AREAGERPALERTHT-TATSQAGDLEK
                                                               568 VSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 AIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMSVIPAIFLVT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISML 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1349;
                                                                                                                                                                                                                                                                                   Drug resistance gene from Aspergillus fumigatus useful for determining fungal multiple resistance inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.3%; score 1956; DB 20; Best Local Similarity 35.8%; Pred. No. 1.7e-173; Matches 491; Conservative 229; Mismatches 478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESEKPRPNQDGSESSHPPP-EKETEGSISD-------
                                                                                                                                                                                                                                                                                                                                       Claim 3; Columns 21-28; 25pp; English.
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                                                                                                  96US-0612734
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                                                                                                                                                                                                                                                    N-PSDB; AAX60201, AAX60202.
                                                                                                                                                                  & CO ELI.
                                                                                                                                                                                                   Skatrud PL,
 Aspergillus fumigatus
                                                                                                                                                                                                                                    1999-370499/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1349 AA;
                                                                                                                                                                  (ELIL ) LILLY
                                                                                                  08-MAR-1996;
                                                                                                                                 08-MAR-1996;
                                  US5914246-A.
                                                                                                                                                                                                     Peery RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFST 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404
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                                                                                                                                                                                                                                                The present sequence represents a multiple drug resistance protein, designated attp, which is isolated from Aspergillus nidulans. The attp polymuclectide is used to produce nucleic acid molecules which are useful in diagnostic assays for the detection of atrb polymuclectides. The atrb polypeptide may be used to identify agents which inhibit multiple drug resistance. These agents may be useful for the treatment of fungal diseases. New antifungal compounds may also be identified using the gene disruption or gene replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KETEGSISDYLRIFRYADKY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 FGSELFSIIDKPTQLDPLDPSGKQPEGCLGQIEIQNLAFAYPSRPSAQVLRDFNLTIPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                        30.1%; Score 1940; DB 20;
llarity 36.8%; Pred. No. 5.3e-172;
Conservative 231; Mismatches 483;
                                                                                                                                  Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADESEKPRPNQDGSESS----SHPPPE----
                                                                                                                                                                                               New multiple drug resistance gene atrD
                                                                                                                                  RB,
                                                                                                                                                                                                                         Claim 12; Page 27-32; 35pp; English.
                                                                                                                                  Peery
                                                                                       (ELIL ) LILLY & CO ELI.
(UYWA-) UNIV WAGENINGEN AGRIC.
                                                               97US-0996545.
                                        98WO-US27300
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                                                                                                                                                         WPI; 1999-418917/35,
                                                                                                                                                                                                                                                                                                                                                                                 1334 AA;
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Matches 490; Conserv
                                                                                                                                                                       N-PSDB; AAX85823
                                      22-DEC-1998;
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                                                                                                                                Andrade AC,
            01-JUL-1999
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SALPTOLOEL------ISANFLIYIVVGQHRLEQC-STTSLWMETGPGGCVW
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                                                                                                                                                                                                                                                                                                                                                                                                                             .023 ydifrffycfs-eilfgagsagtyfsfapdmgkaknaaaefrrifdrkpgidnwseegek
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                                                                                                                                                                                              742 FFVVALGNLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQL
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                                                                                                                                                                                                                                                                                                                                                  907 VE---QG----LAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLN---
                                                                                                                                                                                                                                                                                                                                                                                                     ----FISSSWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIRE-TEENKK
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                                                                                        -----KTLHEKAAREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCI-LI
                                      584 VKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQDLGADEQQEHE----
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RGTIFQNIANGFMDEQRDLPRE-KQMELVQKACKASNGDVFINELPNGYETEVGERAGAL 523

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AAW62871 standard; Protein; 1408
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                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for enhancing the secretion of beta-
lactam compounds from a micro-organism that comprises enhancing ABC (adenosine triphosphate (ATP)-binding cassette) transporter activity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC-transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents the P. chrysogenum ABC transporter aal0 protein sequence.
                                                                                                                                                                                                                                                                           Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFVLWFVYLFIGKFVLTYVSTAAITISAIRTTRTLRRVFLECTLRQEVWHFDKQSNGAIA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTLAA 326
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nekpvdkrdsdsaststakehesktpvasdedalyahlpehekdilkgqldappvnisyf 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 30.0%; Score 1934.5; DB 22; Length 1333; Best Local Similarity 35.3%; Pred. No. 1.7e-171; Matches 490; Conservative 226; Mismatches 468; Indels 203;
                                                                                                                                                                                                          Konings WN;
                                                                                                                                                                                                        Bovenberg RAL, Driessen AJM,
Der M, Westerlaken I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SEKPRPNQDGSESSSHPPPEKETEGSIS-----
                                                                                                                                                                                                                                                                                                                        Claim 8; Page 110-112; 116pp; English.
                                                    99EP-0203684.
99EP-0203685.
99EP-0203687.
99EP-0203689.
99EP-0203689.
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99EP-0203692.
99EP-0203693.
                                 2000WO-EP11489
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Schuurs TA, Nieboer M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1333 AA;
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                                                                                      03-NOV-1999;
03-NOV-1999;
03-NOV-1999;
03-NOV-1999;
03-NOV-1999;
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           10-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLEKRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLSTITVLICAATFPGQALLFSRLLT 722
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SRPSAQVLRDFNLTIPAGKTTALVGASGSGKSTMVGLLERWYLPSSGRILLDGLELGQYN
                                                                                                           491 lrwlrgqislvsqepvlfgttiyqnirhgligtrfeheseekikellenaakmanahefi
                                                                                                                                                                                                                      506 NELPNGYETEVGERAGALSGGQRQRIAIARSIISDPKILLLDEATSALDPKAEKVVQEAL
                                                                                                                                                                                                                                                                                                                                     NRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELIEFGCHYAALVRAQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FKADVDHFVLWFVYLFIGKFVLTYVSTAAITISAIRTTRTLRRVFLECTLRQEVW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSAFVVALASQWKLALITMSV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVHAFYAQKKMVEKYDVFL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGEVADVGKVFTVVLSVTL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.7%; Score 1789.5; DB 19; Length 1408; ilarity 34.4%; Pred. No. 7.9e-158; Conservative 214; Mismatches 493; Indels 203; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PPEKETEGSI----SDYLRIFRYA 41
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                                                                                                                                                                                                                                                                       Dna encoding multiple drug resistance protein of Cryptococcus neoformans - also related vectors and transformed host cells, method for expression of the protein
                                                                     protein; CneMDR1; identification;
                                                Multiple drug resistance protein called CneMDR1
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                                                                                                                                                                                                                                                                                                              Claim 1; Columns 17-26; 19pp; English
                                                                                                                                                                                                                        Thornewell
                                                                             antifungal compound; resistance
                                                                                                                                                            96US-0612521
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                             (first entry)
                                                                     resistance
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                                                                                                 Cryptococcus neoformans.
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                                                                                                                                                                                                                                                                                                                                                                                            1408 AA;
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                                                                   drug
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                                                                   Multiple
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1221 vtldgidikelnlasyrsgislvsgeptlyagtirfnillgankpi-eevtgdeidaack 1279 ERLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEM 1254 563 687 621 ALNRVSKDRTTLVIAHKLATVKSAGNIAVISQGKIVEQGTHHELI - - EPGCHYAALVRAQ DL-----KA 807 aeevage------thyp---ssfglyarllrmnsadkfly---ita 700 TITVLICAATFPGQALLFSRLLTVFELSG-----HAAQERADFYILMFFVVALG----LQELISANFLIYIVVGQHRLEQCSTTSLWMETGPGGC------VWCTSTPAF--854 -GWL------PQNSSRDEARSRKLGKLCRKCWACKRSSYRDPDRLIFDSRRPCSPTVL GHVEQGLAKIIQSFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWL---QVSTTQLNFISS PVDLEDIEFRYRQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGR ISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLALEAELSEELCQGRLPAR--1136 -PMLWILSSLYQKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQS 445 YNVKWLRSRIRLVQQEPVLFRGTIFQNIANGFMDEQ-RDLPREKQMELVQKACKASNGDV 640 AREAAGERPALERTHTTATSQAGDLEKRKVPVGTLGYSLLKCILIMFYEQKNLYWCFLLS -NLVGYFTIGWTCNVISQVVTHRYQAAMFQRVLDQDIELLDIPEQISGALTSQLSALPTQ SWAFCLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPTIR-ETEENK---KKGPVGGC 1255 CLAQSLDQ 1262 1400 vqmqnlsr 1407

AAR99255 standard; Protein; 1307 AA

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malgf------wyggsllghgeyslfgfyvcfsevif--gagaagtvfshapdmgkakha 1030
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          SGKSTMVGLLERWYLPSSGRILLDGLELGQYNVKWLRSRIRLVQQEPVLFRGTIFQNIAN 474
                                                                                                                                                                                                                                                                                                   tvvsltmetealgsygaqlrrqlksdilpivkssll------yassgalpfc
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                                                                             -----WCFLLSTITVLICAATF-PGQALLFSRLLTVFE---LSGHAA
                                                                                                                                                                                                                                                                                                                                                                                            792 QISGALTSQLSALPTQLQE.----LISANFL---IYIVVGQH-----RL
                                                                                                                    AIARSIISDPKILLLDEATSALDPRAEKVVQEALNRVSKDRTTLVIAHKLATVKSAGNIA
                                                                                                                                                                                       GFMDEQRDLPREKOMEL---VQKACKASNGDVFINELPNGYETEVGERAGALSGGQRQRI
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                                                                                                                                                                                                                                                                                                                                                                                                                     A new multiple drug resistance (MDR) protein (AAR99255), designated AfI-WDR1, of Aspergillus flavus was identified as the product of a cDNA clone isolated from a mycelial cDNA library of A. flavus AfI-MDR1 can be synthesised by host cells, partic. Saccharomyces cerevisiae, transformed with vectors that provide for the expression of DNA encoding AfI-MDR1. Transformed host cells can be used to identify cpds. that inhibit fungal MDR activity.
                                                                                                                                                                                                                                                                                                                                                     New multiple drug resistance gene of Aspergillus flavus – used to identify cpds. that inhibit fungal multiple drug resistance activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KPRPNQDGSESS-----SHPPP----EKETEGSISDYLRIFRYADKYDWTLNVIALICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VQALSMFFSAFVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1307;
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                                                                 Aspergillus flavus multidrug resistance protein Afl-MDR1.
                                                                                          Multiple drug-resistance; MDR; Afl-MDR1; antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 1780; DB 17;
34.3%; Pred. No. 5.4e-157;
ive 222; Mismatches 500;
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 22-27; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466; Conservative 222;
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                                       (first entry)
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N-PSDB; AAT35230.
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                                                                                                                    Aspergillus flavus
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           AAR99255;
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                                                                                                                                                      are present compared
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bloavailability of compound and increasing PGP transporter activity in
                                        Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
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to PGP variant AAB81064"
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           P-glycoprotein variant 2.
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                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bloavailability of compound and increasing PGP transporter activity in cell -
                                                                                                                            Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%; Score 1654.5; DB 22; Length 1280; 32.5%; Pred. No. 3.2e-145; tive 253; Mismatches 496; Indels 135;
                                                                                                    P-glycoprotein variant 1.
                                                                                                                                                                                                                                                                                                                                     Crespi CL;
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                          Protein; 1280
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99US-0158818
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                                                                                                    monkey
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12-OCT-1999;
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                  QVVTHRYQAAMFQRVLDQDTELLDIPEQISGALTSQLSALPTQLQELISANFLIYIVVGQ
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                                                                                                                           PEGCLGQ1E1QNLAFAYPSRPSAQVLRDFNLT1PAGKTTALVGASGSGKSTMVGLLERWY
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VALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRTVH 248 

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The present invention describes a recombinant or isolated nucleic acid (1), derived from a prokaryotic gene, which encodes at least a specific and/or functional part of a transporter protein (TP), or its derivatives, which has functional and/or structural similarity with the Pulycoprotein (PS) encoded by the human multidrug resistance (MDR)1 gene. The present sequence represents the human MDR1 protein, derived from MDR1-n and MDR1-cas shown in the specification in flughts 1. (1) is used to express recombinant proteins; its fragments of related DNA. The protein produced, or cells expressing them, are used to determine if substances can inhibit, or avoid, MDR proteins, cand in a screening method for identifying compounds that inhibit transport of cytotoxic substances from cells. Also, cells with a transmembrane protein, especially where expressed from (1), can provide mechanisms of action of PG.
                                                                                                                                          Human; multidrug resistance P-glycoprotein; MDR1; prokaryotic homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prokaryotic homologue of human multiple drug resistance protein - used to screen for compounds that inhibit, or avoid, drug resistance
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                                                                                                                 Human multidrug resistance P-glycoprotein MDR1
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1..640
/note= "MDR1-N from Fig
641..1280
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                          AAW44073 standard; protein; 1280 AA
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RESULT 1
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547 555 607 615 653 703 718 828

881

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966 CLPVQAAAQYLAYSTSFTKARSAANYILWLRTLKPJI--RBTEENKKKGPVGGCPVDLE- 1022
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                                               || ||| ||| :||: ||: || ||| : :|| afggqkkelerynknleeakrigikkaltanisigaafiliyasyalafwygttlvlsge 325
            AFYAQKKMVEKYDVFLQQAHQEGKKKSPNNGVLFSTEYFCIYAAIALAFWKGFRMYQNGE 308
                                                                                                                              VADVGKVFTVVLSVTLAATSISMLAPSGSVVYQRRIFGSELFSIIDKPTQLDPLDPSGKQ 368
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Local Similarity es 428; Conserv

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cells are useful in bone marrow transplattation (to reconstitute hamaropoietic systems in patients who have undergone chemotherapy or radiation therapy) and in ex vivo gene therapy of genetic defects in cells derived from haematopoietic stem cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or leukaemia. The modified cells can also be used to identify factors involved in regulating proliferation and differentiation in haematopoietic stem cells. Haematopoietic stem cells that express MDR-1 will be protected against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multidrug resistance; MDR-1; P-glycoprotein;
transmembrane efflux pump; haematopoietic stem cell; transduction;
bone marrow transplantation; chemotherapy; radiation therapy; cancer;
gene therapy; gene replacement; genetic defect; thalassacmia;
Gauchier's disease; sickle cell anaemia; leukaemia; ex vivo expansion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents human wild-type multidrug resistance protein MDR-1. MDR-1 is a transmembrane efflux pump, responsible for the export of drugs from certain cells, particularly cancer cells. Wild-type MDR-1 shows increased resistance to etoposide and decreased resistance to vinca alkaloids compared with a mutant form (AAYSB187) where the Gly at position 185 is replaced by Val. The invention relates to transducing heamatopoietic stem cells with nucleic acid encoding an MDR protein and culturing the modified cells. The modified haematopoietic stem
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chemotherapeutic agents, so can be engrafted while the patient is undergoing chemotherapy. Expansion of (rare) haematopoietic stem cells provides sufficient cells to permit standard blochemical analysis. Overexpression of MDR-1 allows cytokine-driven expansion of haematopoietic stem cells by at least 10-fold compared with a maximum
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                                                                                                                                                                                                    RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMC 1255
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hypercholesterolaemia; hypocholesterolaemia; atherosclerosis;
coronary artery disease, cerebral vascular disease.
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treatment of cholesterol-related diseases, including hypercholesterolaemia, hypercholesterolaemia, atherosclerosis, coronary artery disease and cerebral vascular diseases. The present sequence is the human MDR1 protein.
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bb 882 qalkdkkelegagkiateaienfittvsltqeqkfehmyaqslqvp 927  Oy 917SFWFGRCFGFHLSQSMEFLAIALGFCIAVDNWLQVSTTQLNFISSSWAF 965  bb 928 yrnslrkahifgitfsftqammyfsyagcfrfgaylvahklmsfedvllvfsav 981  Oy 966 CLPVQAAAQYLAYSTSFTKARSAANYILMLRTLKPTIRETEENKKKGPVGGCPVDLE-1022  Oy 966 CLPVQAAAQYLAYSTSFTKARSAANYILMLRTLKPTIRETEENKKKGPVGGCPVDLE-1022  Oy 1023DIEFRYRGRDSANVLRGYSMITMINiektplidsyste	1094 vildgkelkrinvqwlrahlgivsqepilfdcslaeniaygdnsrvvsqecivraakean 1136 PMLWILSSLYQKALKRLAAQRGWQFSGQQRQRIATARALIRNPKLLLLDEATSALDTQSE 1136 Inafieslpnkystkvgdkgtqlsgqqkqrialaralvrqphillideatsaldtese 1196 RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIEVFANGRIAETGTHAELQRERGRYYEMC 1196 RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIEVFANGRIAETGTHAELQRERGRYYEMC 1212 kvvqealdkaregrtcivlahrlstignadlivvfqngrvkehgthqqllaqkglyfsmv 1256 LAQS 1259 1: 1	RESULT 14 AAR04868  ID AAR04868 standard; protein; 1280 AA.  XX AC AAR04868;  XX  AX  AND BE Protein encoded by Multidrug Resistance Al gene.  XX  WW Multidrug Resistance Al gene; drug resistance of cancer cells; ss.  XX  NX  NM  Nultidrug Resistance Al gene.  XX  NX  NM  Nultidrug Resistance Of cancer cells; ss.  XX  NX  NX  NX  NX  NX  NX  NX  NX  N	Proceedings of the process precific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence, used for diagnosing drug process specific amino acid sequence cells.  XX Cr The gene that encodes this protein is useful for diagnosis of drug cresistance of cancer cells.  XX Soquence 1280 AA; Soquence 1280 AA; Sourcer Match  Query Match  Query Match  Dest Local Similarity 32.3%; Pred. No. 1.4e-144;

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This invention relates to a polynuclectide sequence encoding a cynomologous monkey P-glycoprotein (PGP), and an allelic variant of the GPP protein. PGP, also known as multidrug transporter. MDR1 is a member of the ABC transporter superfamily. The enzyme serves as an efflux pump exporting small molecules across the cell membrane. The invention includes a cynomologous monkey (Macaca fascicularis) PGP coding sequence and protein, and also that of an allelic variant. The PGP polynucleotide sequence is useful for increasing PGP transporter activity in a cell. Antisense sequences of the cDNA are useful for inhibiting PGP transport activity in a mammalian cell. They may also be used for increasing the bloavailability of a drug. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                  1078 ISFAHENIAEMSPRLYRGHMSLVQQEPTLYQGSVRENVTLALEAEL--SEELCQGRLPAR 1135
                                                                                                                                                1196 RLVQAALDEASTSRTTIAVAHRLSTIRNVDVIFVFANGRIAETGTHAELQRLRGRYYEMC 1255
                                                                                                                                                                                                                                                                                                                                                                         1023 ----DIEFRYRQRDSARVLRGVSMTIEPGQFVAYVGASGCGKSTLIALSERFYDPTSGR 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monkey; P-glycoprotein; PGP; multidrug transporter; MDRl;
                                                                                                                                                                                                                           1136 PMLWILSSLYOKALKRLAAQRGMQFSGGQRQRIAIARALIRNPKLLLLDEATSALDTQSE
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efflux pump;
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12-OCT-1999;
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                                                                                                                                                        TRTLRRVFLECTLRQEVWHFDKQSNGAIATXVTTNGNRIQTGIAEKLVFTVQALSMFFSA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                  615 elmkekgiyfklvtmqtrgnelelen----atgesksesdalemspkdsgsslikrr 667
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                                                                                                                             rnktfpviinesitnntghfinhleeemttyayyysgigagvlvaayiqvsfwclaagrq 144
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                                                    EKETEGSISDYLRIFRYADKYDWTLNVIALICAIGSGASLPLMSIIFGSFTNKFNNYNSG
                                                                   FVVALASQWKLALITMSVIPAIFLVTGICIAIDAAQEARITRIYSRAAVLAEEVLSSIRT
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 Length 1280;
25.5%; Score 1643.5; DB 22; Length 1280
llarity 32.2%; Pred. No. 3.4e-144;
Conservative 246; Mismatches 504; Indels 141;
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              al Similarity
423; Conserv
  Query Match
Best Local S
Matches 423
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG646725 687 bp mRNA linear EST 24-APR-2001 EST508344 HOGA Medicago truncatula cDNA clone PHOGA-9L3 5' end,
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/clone_lib-"HOGA"
/tissue_type-"3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
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H1716519
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1 atggcagatgaatcggagaa.....aatctttagaccaagcatga 3792
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Entamoeba histolytica HM1:IMSS sheared

USA

MD 20850,

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/organism="Entamoeba histolytica"
/strain="MillimSs"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Librk,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
/75450.), The DNA was mechanically sheared to give a
fight size distribution (-2 kb). The v + 1 method used for
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                              Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 897)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  togacotogaggacattgaattcaggtatcgtcaacgtgattcggctcgagttctccgcg 3115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 TACCTAAAGGAGTTGAAGTAAGTAATGAACAAATTTATGCTGCTGCTAAAATGGCAAATG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tggtccaacaggaacccacatttaccaaggctccgttcgcgagaatgtga----cgttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 168; DB 12; Length 897;
Similarity 53.9%; Pred. No. 1.8e-39;
11; Conservative 0; Mismacches 330; Indels
                                                                                                                                                                            Unpublished (2000)
Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
7813 01838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba
DNA library
DNA library
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start:
High quality sequence stop: 8
Location/Qualifiers
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Matches 391;
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                                                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Xhoi; CDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap RN vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 bp DNA linear GSS 14-NOV-2000 genomic, DNA sequence.
AZ541090.1 GI:111484493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 TATGG - TAAAGGAGGAGATGCATCAGAGCAGAGATTATAGCTGCAGAAATTAGCA- 360
                                                                                                                                                                                                                                                                               Score 169.4; DB 10; Length 687;
Pred. No. 5.6e-40;
0; Mismatches 296; Indels 21; Gaps
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AKO14319

Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:322401P09:ATP-binding cassette, sub-family B (MDK-TAP), member 8, full insert sequence.

AKO14319.1 GI:12852089
H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                              Score 167.4; DB 12;
Pred. No. 2.7e-39;
0; Mismatches 331; I
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Best Local Similarity 53.8%;
Matches 391; Conservative
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Entamoeba histolytica.

Entamoeba histolytica

Eukaryota; Entamoebidae; Entamoeba.

I (bases 1 to 886).

Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Fraser, C.

Loftus, B., Mang, Z., Van Aken, S. and Library (2001)

Loftus Genomic Research

Fra: 301 838 0208

Fax: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI: IMSS sheared

DNA library
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ENTNA47TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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        ctttggattttgtcatctttaccagaaggetttgaaacgccttgcggctcaacgaggg 3471
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                                                               464 CACATGACTTTATTTCAGCAATGCCAGAAGGATATAACAC-AATGGTAGGTGATAGAGGT
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YTRDHMGSFVSESRKLSVQLLILYGVQCILTPGYLVLISHIOERWADWRKALFSSLL
RQDIAFFDAKKTGQLVSRLTTDVQEFKSFFKLVISGGLRSCTQVIGSLVSLSMLSPRL
TLMIAVVTPALMGVGTLMGSGLRKLSRQCQEQIARATGVADEALGGVTVRAFAMERR
BEBRYQADELSSCCGCAREEGGRIALBGCGCATARATGVADEALGGVTGSLVSTRUDI
RGSITFQNVTFSYPCRFGFNVLKDFTLKLPSGKIVALCGFLGTGGSLVAGQQUKGGD
LMGSTVASGTVQRSWASLSVLFGQVVRGLSAGANVFFYWALSPYIPTGSCYCIPNRDI
RGSITFQNVTFSYPCRFGFNVLKDFTLKLPSGKIVALVGGSGGGKTTVASLLERFYDP
RAGSYVCDFULDKTLMRSWLRGQVYGTSGROPVLEATT MENINTRYKLDADSDEVYTA
ARENNAMEYISSPPCYSTVVGERGTTLKLSGCGCORQURATARANICKOLDSDETSYTA
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ARENNAMEYISSPPCYSTVVGERGTTLKGVGCTTHERLLNKG
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//de/_stage="14, 17 days embryo"
72. .2225
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/note-"ATP-binding cassette, sub-family B (MDK/TAP),
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/db_xref="taxon:10090"
/clone="3222401P09"
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/note="putative"
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

5 (bases 1 to 2676)

5 (bases) to 2676)

6 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arawa, T., Baldarelli, R., Beno, H., Furuno, M., Hanagaki, T., Hara, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, P., Hayahi, R., Hayaki, T., Hara, P., Hayahish, N., Ishil, V., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Nomura, K., Nomura, K., Nomuzaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, X., Shibata, Y., Shinaqawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Yamamura, I., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Sabhata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kohibata, K., Itoh, M., Aisawa, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Sumi, N., Ishi, Y., Inoue, R., Sakaguchi, S., Ikeqami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Rike integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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HTC: CAP trapper.
Mus musculus (strain:C57BL/6J) 14, 17 days embryo head cDNA tc
MRNA, clone_1lb:RIKEN full-length enriched mouse cDNA llbrary
clone:3222401P09.
                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 9279253
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947 bp DNA linear GSS 14-DEC-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Eukaryotts Intemoebidae; Entamoeba.

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:HMSS sheared DNA library
LU Unpublished (2000)

Contact: Brendan J. Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 043
Email: Djloftusetigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
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/strain="HAM:IMSs"
/db_xref="HAM:IMSs"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (FIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Dlamond (Clark, C.G., and Dlamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
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                                                                                                                    cgaacggttatgagactgaagttggcgagcgagccggagccttgagtggaggtcaacgac
                                                                                                                                                   1810 ccGATGGCTACAGCACTGTGGTTGGTGAGCGGGCACAACCTTGTCTGGTGGCCAGAAGC
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BNTCR5OTR Entamoeba histolytica
genomic, DNA sequence.
A2532602
A2532602.1 GI:11088090
GSS.
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Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 19
High quality sequence stop: 801.
Location/Qualifiers
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Entamoeba histolytica
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/Strain-"Hurilans-
/db_xref"-taxon:759"
/db_xref"-taxon:759"
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/clone_lib="Entamoceba histolytica Stockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark,
C.G., and Diamond. L.S. (1993) Entamoceba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for whole genome shorgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barall, Oxford University Press, 1999)."
Eukaryota: Entamoebidae: Entamoeba.

(bases 1 to 947)

(contus, B., Van Aken, S.

(contus, B., Van Aken, S.

(contus, B., Van Aken, S.

(contact: Brendan J Loftus

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/strain="Mai.IMSs"
/db_kratin="Mai.IMSs"
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/note="vector: pHOS1; Site_li BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + I method used for
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
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the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell. Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 TCAGGATGTGGGAAGTCAACTACTATTCAATTAATCCAAAGAAATTATGATCCAAATGGT 317
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                                                                                                                                                                Length 871;
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Survivat 919 bp DNA linear GSS 14-DEC-2000 ENTIY66TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence. A2690701

LOCUS DEFINITION ACCESSION VERSION

RESULT AZ690701

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/burne_ini_tmin_tmss."
/db_xref="taxon:5759"
/doc_xref="taxon:5759"
/clone_lib="Entemboba histolytica Sheared DNA"
/clone_lib="Entemboba histolytica Sheared DNA"
/clone_weetor: pH051; Site_1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, WD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter. J.C. (Making small insert librarles for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Pred. No. 1.9e-37;
0; Mismatches 316; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MD 20850, USA
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/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                        Entamoeba histolytica
Enkaryota: Entamoebidae; Entamoeba.
1 (bases 1 to 919.
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from the sequences of the sequence of the sequences of t
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Best Local Similarity 53.2%;
Matches 376; Conservative (
histolytica
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Entamoeba
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COMMENT
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A2548312
B34 bp DNA linear GSS 14-NOV-2000 ENTEGOTRE Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
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                                                                                                                                                                                                                                                                                      203 CGGTGACGTTGGATGGCCATGACCTGCGAACTCTCAACCCCTCCTGGCTCCGGGGCCAGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                        263 TCATAGGTTTCATCAGCCAGGAGCCAGTCTTGTTGTAACAACAACATGAGAATATCC 322
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                                                                                                                                                                   23 GTAACATCACCTTCCAAAATGTCACCTTCAGCTACCCCTGCAGACCTGGCTTCAATGTGC
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                                                                 815;
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 others
                                                                   Length
 -
                                                                Score 160; DB 10;
Pred. No. 4.7e-37;
0; Mismatches 315;
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 163
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GSS.
Entamoeba histolytica.
Entamoeba histolytica
Eukaryota: Entamoebidae; Entamoeba.
1 (bases 1 to 834)
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Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Clume is a column: 07

High quality sequence start: 28

High quality sequence stor: 808.

Location/Qualifiers

ree
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602961127F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5116782 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                            1626 gatectgitactegatgaagetaceagegeectigaeeegaaggegagaaagtggieea 1685
                                                                                                                                                                                                cotottcattaatgagetteegaacggttatgagaetgaagttggegagegageeggage 1565
                                                                                                                                                                                                                                                                    cactgicaaaagigciggcaacaicgcagicatticccaggggaaaatcgicgagcaagg 1805
                    381 TGACTTCATTTCAGCAATGGCAGAATATGACACAATAATTGCAGATAGAGGTGCACA 440
                                                                              441 AATTTCAGGAGGACAGAAACAAAAGAATTGCACTTGCACGTGCATTGATTAGAAATCCAAA 500
                                                                                                                                                                                                                                                                                          621 GACTATICAAAAIGCAGATCAAATATGIGITATIAIGAGAGGAAAAIIAGTAGAAAAGG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 815)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                              1566 cttgagtggaggtcaacgacaacgaattgcaatcgcacgaagtatcatatcggatcccaa
                                                                                                                                                501 AGTGTTATTACTTGAAGGTACATCAGCACTTGATACACAAAAGTTGTACA
                                                                                                                                                                                                                                                                                                                              1806 cacaccaccacgaattgatcgaattcggctgtcattacgccgcactgg 1852
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ACCESSION VERSION KEYWORDS SOURCE

BI409057

RESULT

REFERENCE

FEATURES

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3772 caatct 3777
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Entamoeba histolytica"
/strain="Man:IMSS"
/db xref="taxon:579"
/db xref="taxon:579"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/rofe="vector: pHOSI; Site_l: BSt !; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S.
(1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
/7:500.) The DNA was mechanically sheared to give a
flight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotyun sequencing projects. In Genome
Sequencing: A practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                 Determination of close and sequences from Entamoeba histolytica Determination of close and sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
L Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Emai: bloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M3-Reverse
Class: shotgun
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Van Aken,S. and Fraser,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 GTATTTCATTCAAAGCAGAACAAGGGAAAACAATTGCATTAGTTGGAGCATCAGGATGTG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 TATTAGATGGACATAATAFCAAAGATTTAAATATTCATTTCTTAAGAAATCAAATAGGAT 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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High quality sequence stop: 830.
Location/Qualifiers
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Best Local Similarity 53.23
Matches 386; Conservative
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1...906
/organism="Homo sapiens"
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/note="vector: pcMx9PorT 6; Site_1: NotI; 1st strand cDNA
/note was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
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/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the pcMvSPORT 6
/cloned into the Not I and Eco RV sites of the PcMvSPORT 6
/cloned into the Not I and Eco RV sites of the PcMvSPORT 6
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AL578780 AL578780.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 906)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA lbraries and normalization
Unpublished (2001)
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ccaaagctgttgctacttgacgaagcgacgtcagccctcgacacgcaatcggaacgtctg 3591
                                                                                                                                                                                                                                                                                                                                                                                                                                    3652 ctttccactattcggaatgttgatgttattttttgtgttttgccaacgggagaatcgccgaa 3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 27; Gaps
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edenoscope - Centre National de Sequencage
Benoscope - Centre Cedex - France
Bp 191 91006 EWRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                            643 GTACAAGATGCACTTGACAAAGCATCAAAAGGAAGAACAACAATTGTAATTGCACATAGA
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4.0%; Score 151.6; DB 9;
Best Local Similarity 53.7%; Pred. No. 1.9e-34;
Matches 378; Conservative 0; Mismatches 299;
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/roce="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Ollgo dT.
Average insert 2 kb. Library constructed by Life
Average insert 2 kb. Library constructed by Life
Average insert 2 kb. Library constructed by Life
for transgenic model: x et al., Nature Genetics 22, 37-43
(1999). Note: this is a NCL CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1490 aagccagcaatggcgacgtgttcattaatgagcttccgaacggttatgagactgaagttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%; Score 150.4; DB 10; Length ilarity 54.1%; Pred. No. 3.7e-34; Conservative 0; Mismatches 286; Indels
Location/Qualifiers
1. .667
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Matches 369; Conserv
                                                                                                                                                                                                                                                                                                                                                                  139
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                             source
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I (bases 1 to 667)

NH-MCC http://mgc.nci.nih.gov/.

NH-MCC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1471 cttgtgcaaaaagcttgcaaagccagcaatggcgacgtgttcattaatgagcttccgaac 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1531 ggttatgagactgaagttggcgagcgagccggagccttgagtggaggtcaacgacaacga 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1711 gaccgcactactttggtcattgcccacaaaactagccactgtcaaaagtgctggcaacatc 1770
gcatcaggtagcggcaaaagcacaatggtcggcttacttgaacggtggtatctgcccagt 1293
                                                                                             tcggggaggatattacttgatgggttggaactgggacaatacaatgtgaaatggctgaga 1353
                  844 CAGTCTGGGGAAGAAGACCACCGTGGCTTCCTGCTGGAGCGCTTCTACGACCCCACG 785
                                                                                                                                                                                                                                     724 Geccaggirgrescritcarcascrassascescreteririsseaccarcarcarssas 665
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                                                                                                                                                                                                                                                                                                                                  1831 ggctgtcattacgccgcactggtgcgtgcacaggacctcggggc 1874
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BI652986.1 GI:15567222
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Entamoeba histolytica.

Entermination of clone end sequences from Entamoeba histolytica.

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                                                                                                                                                                                                                                                                                                        1343 aatggetgagaageegeattegeetegtteaacaggaaeetgtgttgtttegtggeaeaa 1402
                                                                                                                              1403 tettecagaacattgecaaeggttteatggatgageaaegagatetgeetegegaaaae 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AATGGTTAAGAAATCAAATAGGAATAGTTGGACAAGAACCAGTATTATTTCAGGAACAA 383
                                                                                                                                                                          384 TIGGAGAAAATATCAIGCITGGAGCIAAAGAAGGAGAA--------ACACIAA 428
                                                                                                                                                                                                                                                                  429 GTAAAGAAGAGATGATTGAATGTACTAAAATGGCAAATGCACATGACTTTATTTCTAAAC 488
264 ATGAACCAAATGGTGGAAGAGTAACATTAGATGGGAAAGACATAAGAGAGTTGAATATCA 323
                                                                                                                                                                                                                                                                                                                                                                                                                             1643 aagctaccagcgcccttgacccgaaggcggagaaagtggtccaggaggccttgaaccgag
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High quality sequence stop: 627.
Location/Qualifiers
1.921
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/db_xref="taxon:5759"
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A2687628
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/db_xref="taxon:5759"
/doc_lib="Entaxon:5759"
/clone_lib="Entaxoneba histolytica Sheared DNA"
/clone_lib="Entaxoneba histolytica Sheared DNA"
/clone_lib="Meacor: pH051; Site_l: Bst 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitolytica: a method for isolate identification Exp. Parasitolytica: a method for isolate identification by expression of the library construction is described in detail in Smith, H.O. and Venter. J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing. A practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                        BH154857 899 bp DNA linear GSS 24-SEP-2001
ENTRO47TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Brendan J Loffus
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Eax: 301 838 3543
Enail: bjloftusetigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
                                                                                                                                                    Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 899)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI: IMSS sheared DNA library (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 GACCATCTCATCATGTATTAAAAGGAATTGACCTTGAAATTAAGAAAGGAGAAATAATTG
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Pred. No. 4.4e-34;
0; Mismatches 386; Indels 16;
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/strain="HM1:IMSS"
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High quality sequence stop: 787.
Location/Qualifiers
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                                                                                                               BH154857.1 GI:15726574
                                                               genomic, DNA sequence.
BH154857
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Best Local Similarity 51.0%;
Matches 418; Conservative
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="weetor: pHoS1; Site_1: Bst !; Constructed at The
Institute for Genomic Research (TIGR). Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Entamoeba histolytica.

In (bases it of 84.2)

Secretarination of clone end sequences from Entamoeba histolytica.

Hill INSS sheared DNA library

Contact: Brenden J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 34.3

Email: bjloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Reverse

Class: shotgun

High quality sequence start: 19

High quality sequence start: 839.

Location(Qualifiers)
842 bp DNA linear GSS 14-DEC-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
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          ENTMN93TR Entamoeba hl
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Matches 375;
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qq	537	ACACTAAGTAAAGAAGAGATGAATGTACTAAAATGGCAAATGCACA	488
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April 27, 2002, 01:37:27 ; Search time 96.68 Seconds (without alignments) 7205.145 Million cell updates/sec
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Database :

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NO.	Score	Match	Length DB	DB	QI	Description
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2	259	6.8	4643	9	US-10-097-340-1	
m	133.2	3.5	1839	Ŋ	US-09-540-209B-1731	173
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'n	98.8	2.6	648	Ŋ	US-09-540-209B-1067	
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œ	92	2.4	~	'n	US-09-540-209B-527	527,
σ	82	2.2	721	9	US-10-105-299-238	238,
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17	62	1.6	270	S	US-09-975-254-17150	
18	•	1.6	1827	ហ	US-09-540-209B-1069	
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22	48.8	1.3	1985	7	US-60-365-384-362	362, p
23	47.2	1.2	729	S	US-09-540-209B-4933	4933,
24	46.2	1.2	675	Ŋ	US-09-540-209B-2672	
25	45.2	1.2	244	Ŋ	US-09-975-254-25671	Sequence 25671, A
c 26	43.8	1.2	207	S	US-09-540-209B-4408	Sequence 4408, Ap

RESULT PCT-US	RESULT 1 PCT-USO2-07826-1
. Se	Sequence 1, Application PC/TUS0207826 GENERAL INFORMATION:
<b>4</b> 1	APPLICANT: Millennium Pharmaceuticals, Inc. et al.
	TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND FIOCEINS FOR THE LUBERLINGALION, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
	FILE REFERENCE: MRI-030PC
	CURRENT APPLICATION NUMBER: PCT/US02/07826
	CURRENT FILING DATE: 2002-03-14
	RIOR APPLICATION NUMBER: 60/2/6,025
	PKTUK FILING DATE: JOUL 03-14 DBFOD ADDITORATON NIMBED, KOA355 149
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.,	PRIOR APPLICATION NUMBER: 60/311,/32
	PRIOR FILING DALE: 2001-10-10-10-
<b>μ</b> Ω	PETICO FILITIO DAMPE: 2001-200
	PRIOR FILING DATE: 2001-09-19
	NUMBER OF SEO ID NOS: 363
S	SOFTWARE: FastSEQ for Windows Version 4.0
; SE	SEQ ID NO 1
••	LENGTH: 4643
٠.	TYPE: DNA
٠.	ORGANISM: Homo sapiens
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o e	Ouery March 6.8%; Score 259; DB 1; Length 4643; PBest Local Similarity 44.9%; Pred. No. 1.8e-70; Marches 1517: Conservative 1: Mismarches 1821; Indels 66; Gans 12:
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us-09-882-694a-10\_1.rnpn

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APPLICANY: Karen GLATY
APPLICANY: Karen GLATY
TTTLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TTTLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REPERENCE: MIL.03
CURRENT APPLICATION NUMBER: 05/10/097,340
CURRENT FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
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PRIOR PRIOR SEQ ID NOS: 363
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Best Local Similarity 44.9%; Pred. No. 1.8e-70;
Matches 1537; Conservative 1; Mismatches 1821; Indels
                                                                            ; Sequence 1, Application US/10097340; GENERAL INFORMATION:
; APPLICANT: John MONHAN
; APPLICANT: Manjula GANNAVARAPU
                                                                                                             John MONAHAN
Manjula GANNAVARAPU
Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
                                                                                                                                                                                                                                                                                                                        Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                 Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                       Peter VEIBY
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Karen GLATT
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ORGANISM: Homo sapiens
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10S-50-209B-1731
Sequence 1731, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES FITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1001-001 CURRENT APPLICATION NUMBER: US/09/540,209B CURRENT FILING DATE: 2000-04-04 NUMBER OF SEQ ID NOS: 10444 SEQ ID NO 1731
                                                                                                                                                                             DB 5;
                                                                                                                                                                                                         348;
                                                                                                                                                                             Score 133.2; DB 5
Pred. No. 2.2e-31;
0; Mismatches 348
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Similarity 51.0%;
58; Conservative (
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US-09-540-209B-1731
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Best Local Simi
Matches 368;
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US-09-540-209B-966
Sequence 966. Application US/09540209B
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 966
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                                                                                                                                                                                Length 648;
                                                                                                                                                                             Score 98.8; DB 5; Length 6 Pred. No. 7e-21; 0; Mismatches 152; Indels
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55.8%; Pred. No. 2e-20;
tive 0; Mismatches 148;
2000-04-04
                                                                                                                                                                                Query Match
Best Local Similarity 55.6%;
Matches 190; Conservative
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Best Local Similarity 55.8'
Matches 187; Conservative
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 1067
                                                                              ; TYPE: DNA; ORGANISM: B.fragilis
US-09-540-209B-1067
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; ORGANISM: B.fragilis
US-09-540-209B-966
                                                           LENGTH: 648
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            APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709:1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
LENGTH: 2223
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
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                                                                                                                                                                                                                                                                                                    Length 2223;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                Score 100.2; DB 5;
Pred. No. 5.1e-21;
0; Mismatches 313;
                                                                                                                                                                                                                                                                                                2.6%;
                                                                                                                                                                                                                                                                                              Query Match 2.6%
Best Local Similarity 49.6%
Matches 326; Conservative
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US-09-540-209B-3205
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US-09-540-209B-1067
                                                                                                                                                                                                   TYPE: DNA
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Sequence 527, Application US/09540209B
GREEAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ 1D NOS: 10444
SEQ 1D NO 527
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                                                                                                     1924 gotgotgoagtaaagtotggggcocatagtitoatototggaotocotoagggotatgao 1983
                                                                                                                                         actgaagttggcgagcgagccggagccttgagtggaggtcaacgacaacgaattgcaatc 1599
                                                                                                                                                                                                                               cccagttcggggaggatattacttgatgggttggaactgggacaatacaatgtgaaatgg 1347
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1168 totgeccaagtacttcgagatttcaacttgacaattccagetggcaagacggccgtc 1227
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                                                                                                                                                                                                                                                                                                             1660 gacccgaaggcggagaaagtggtccaggaggccttgaac 1698
                                 1885 tatggcctgacccagaagccaact----
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US-09-540-2098-527
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-09-540-209B-527
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1120 ggtcaaattgagatccaaaacctggcatttgcctaccctcccgaccatctgcccaagta 1179
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                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA.103PLC1
CURRENT APPLICATION UNDHER: US/10/102,806
CURRENT APPLICATION UNDHER: US/10/102,806
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR RELING DATE: 2002-03-23
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SGCTWARE: PALENTIN VET: 2.0
SED ID NO 308
LENGTH: 2171
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Best Local Similarity 49.6%; Pred. No. 6.7e-19;
Matches 287; Conservative 0; Mismatches 271; Indels
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NAME/KET: misc_feature
CCATION: (2168)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-308
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
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LOCATION: (1248)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (2162)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (2166)
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ORGANISM: Homo sapiens
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US-10-102-806-308
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PRILCANT MUDIEN, SERIES OF URINARY TRACT TISSUE
TITLE REPERCENCE TO 1037 CIP
CURRENT PAPLICANTIN WOMEN TO 10 CO 10
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APPLICATION NUMBER: 60/007,495
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APPLICATION NUMBER: 09/035,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LING DATE: February
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                                                                           1921 cgtttgttgattgctcgtgcgctgtatcgggatccgaaatttctctttatggacgaagcc 1980
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                                                1648 accagogocottgacocgaaggoggagaaagtggtocaggaggoottgaacogagtgtoo 1707
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Pred. No. 1.3e-15;
0; Mismatches 170; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PSS50
CURRENT APPLICATION UNDHER: US/10/105,299
CURRENT APLICATION NUDHER: US/10/105,299
NUMBER OF SEQ ID NOS: 151197
PILOT Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
LENGTH: 721
LENGTH: 721
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Sequence 34545, Application US/09540210B

GENERAL INFORMATION:

APPLICANT: Sellhamer, Jeffrey J.

APPLICANT: Delegeane, Angelo M.
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Best Local Similarity 52.0°
Matches 184; Conservative
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; ORGANISM: Homo sapiens
US-10-105-299-238
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 3403
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                                                                                                                                                                                                                                                                                                                                   Length 807;
                                                                                                                                                                                                                                                                                                                             Query Match 2.0%; Score 75.4; DB 6; Length 8 Best Local Similarity 56.1%; Pred. No. 1.6e-13; Matches 142; Conservative 0; Mismatches 111; Indels
                                                                                                                                                                                      ; LOCATION: (57)..(57)
; OTHER INFORMATION: n equals a,t,g, or
US-10-106-698-2063
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catggtttgcttg 511
                                                                                                                      FEATURE:
NAME/KEY: misc_feature
                                                                   TYPE; DNA
ORGANISM: Homo sapiens
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CORGANISM: B.fragilis
US-09-540-2098-3403
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US-09-540-209B-3403
            SEQ ID NO 2063
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Best Local Si
Matches 322;
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GERERAL INFORMATION:
FOR A PAPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REPERENCE: PAOGOSTI
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: PCT/US00/26524
PRIOR APPLICATION NUMBER: DC 09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PLING DATE: 1999-09-29
PRIOR PLING DATE: 1999-09-29
PRIOR PLING DATE: 1999-109-29
PRIOR PLING DATE: 1999-109-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: rat00136905
U;-099-540-2108-34545
PRIOR FILING DATE: March 4, 1998
PRIOR PILING DATE: March 5, 1997
PRIOR PILING DATE: March 5, 1997
PRIOR PILING DATE: March 12, 1998
PRIOR PILING DATE: March 12, 1998
PRIOR PILING DATE: March 14, 1997
PRIOR PELING DATE: March 1998
PRIOR PELING DATE: May 8, 1998
PRIOR PELING DATE: May 8, 1998
PRIOR PELING DATE: May 8, 1997
PRIOR PELING DATE: May 8, 1997
PRIOR PELING DATE: May 29, 1997
PRIOR PELING DATE: May 29, 1997
PRIOR PELING DATE: May 29, 1997
PRIOR PELING DATE: May 1997
PRIOR PELING DATE: June 30, 1998
PRIOR PELING DATE: June 9, 1998
PRIOR PELING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SEQ ID NO 34445
LENGTH: 304
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Molecules and Other Molecules Associated With
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                                             ctttaccagaaggetttgaaacgeettgeggeteaacgagggatgeagtteteeggeggg
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1.8%; Score 68.6; DB 5;
Best Local Similarity 59.4%; Pred. No. 1.1e-11;
Matches 133; Conservative 0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14965, Application US/09975254
GERREAL INFORMATION:
APPLICANT: BYTUM, JOSEPH R.
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(15309)B
CURRENT APPLICATION NUMBER: US/09/975,254
CURRENT FILING DATE: 1999-03-05
FRIOR FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 31255
LENGTH: 237
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 7009098B7H1
02-09-975-254-14965
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-09-975-254-14965
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US-09-540-209B-968
US-09-540-209B-968
GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT APPLICATION NUMBER: US/09/540,209B
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 968
SEQ ID NO 968
LENGTH: 1725
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                                    1854 catcgattctctttctttggggtataatacgaagatcggcatggagggaaacggcatcag 1913
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            aacaggaacccacactttaccaaggctccgttcgcgagaatgtgacgttggccctcgaag 3361
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                                                                     3362 ccgaattatcagaagagctttgtcaaggacgccttcccgcaaggccaatgctttggattt
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Pred. No. 1.6e-11;
0; Mismatches 339;
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US-09-540-2098-968
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APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Yates, Karen
APPLICANT: Tates, Karen
APPLICANT: Tates, Karen
APPLICANT: Halono, Shuichi
APPLICANT: Misuro, Shuichi
APPLICANT: Glowacki, Julie
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SKELETAL DEGENERATION CONDITIONS
TITLE OF INVENTION: DIAGNOSIS PROFERENCE DOGENERATION CONDITIONS
CURRENT APPLICATION NUMBER: PCT/USO2/07787
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 5011
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Sequence 35, Application PC/TUS0207787 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-07787-35
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US-60-116-14683

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US-08-846-027-3

US-09-067-67-3

US-09-749-340-3

US-09-789-340-3

US-09-789-1386

PCT-US99-20770-1

CUS-09-208-809-1

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Pred. No. 0;
; Mismatches
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US-09-351-224-10
Sequence 10, Application US/09351224
GENERAL INFORMATION:
APPLICANT: DUVICK, Jon
TITLE OF INVENTION:
FILE REFERENCE: 5718-111
CURRENT APPLICATION WUMBER: US/09/351,224
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 10
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 3792; Conservative 0;
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ORGANISM: Exophiala spinifera
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Sequence 10, Application US/09351224E
GENERAL IMPORMATION:
APPLICANT: DUVICK, JON
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: FOLKerts, Otto
APPLICANT: FOLKerts, Otto
TITLE OF INVENTION: Compositions and Methods:
TITLE OF INVENTION: Detoxification
FILE REFERENCE: 5718-111
CURRENT APPLICATION UNMBER: US/09/351,224E
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                    Query Match 100.0%; Score 3791.2; Best Local Similarity 100.0%; Pred. No. 0; Matches 3792; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 11

SOFTWARE: PastSEQ for Windows Version 4

SEQ ID NO 10

LENGTH: 3792

TYPE: DNA

ORGANISM: Exophiala spinifera
FEATURE:

NAME/KEY: misc.feature

LOCATION: (0)...(0)

OTHER INFORMATION: p-glycoprotein, full
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                                             TITLE OF INVENTION: Compositions and Methods FILE REFERENCE: 5718-56 CURRENT APPLICATION NUMBER: US/09/351,823 CURRENT FILING DATE: 1999-07-12 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO.10
                                   US/09351823
                                                                                                     TYPE: DNA
ORGANISM: Exophiala spinifera
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S-09-351-823-10
Sequence 10, Application
GENERAL INFORMATION:
Query Match
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quence 10, Application US/09677488
WHERAL INFORMATION:
PPLICANT: DUVICK, John
TILE OF INVENTION: Compositions and Methods for Fummonisin Detoxification
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FEATURE:
COTHER INFORMATION: p-glycoprotein, fully spliced
3-09-09-677-488-10
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                                                                  Score 3791.2;
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CURRENT APPLICATION NUMBER: US/09/677,488
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 3792
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100.0%;
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ORGANISM: Exophiala
                                                                  Query Match
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1921 cgagaagctgctggtgaacgaccggcacttgagcgcactcacaccgccgcactccaa 	gctggagacttggagaagcggaaggtgccggtcgggactttgggctactcgctcctaaa 	Oy 2041 tgcatcctaatcatgttctacgaacaaaaatctctactggtgcttcttgttgtcaaca 2100 	Oy 2101 ataacggttctgatatgcgcgccacatttccaggacaagccttttgttttcgagattg 2160	Oy 2161 ctcactgtcttcgagttgagtggtcatgcggcacagggaacgggcagacttttatattctg 2220	Oy 2221 atgttctttgtcgtggctctaggaaatctagtaggatatttcacgattggctggacatgc 2280	Oy 2281 aacgttatttcacaagttgtcacccatcgctatcaagccgcaatgttccaacgagtactg 2340	Oy 2341 gatcaagacatcgaactcctgacatcccggagagaaatttctggtgctctcacatcgcaa 2400 	Oy 2401 ctgtcagctctacccacgcagttgcaagagttgatatcagcaaattttctcatttatatc 2460 	Oy 2461 gttgtcggtcaacatcgtctcgagcagtgctctaccactagcctatggatgg	Oy 2521 cctggtggttgtgtttggtgcacttccaccctgcttttggctgctacctcagaattcg 2580	Oy 2581 tctagagacgaagctagaagccggaaactcggcaaactttgcagaaagtgctgggcttgc 2640	Oy 2641 aagcgaagcagttaccgcgatccggaccgtctcatctttgactctcgaaggccatgttct 2700	Oy 2701 ccaacagtactcggacatgttgagcaaggtcttgctaagatcatccaaagcttttggttt 2760 	Oy 2761 ggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgccctggga 2820 	Oy 2821 tittgtattgcagtcgataattggcttcaggtgagtacgacacacac	Oy 2881 tettegtgggegttttgtttgceggtecaageageageccagtatttggettaetecaeg 2940	Oy 2941 agtttaccaaggctcggtcggctgcgaactatatcctctggctgcggacattgaagccg 3000 

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N: Compositions and Methods for Fumonisin
N: Detoxification
5718/204100
ON NUMBER: US/09/677,488A
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. LoCATION: (0)...(0)

...OTHER INFORMATION: p-glycoprotein,

US-09-677-48BA-10
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Best Local Similarity 100.0%;
Matches 3792; Conservative 0;
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                     TYPE: DNA ORGANISM: Exophiala spinifera
NUMBER OF SEQ ID NO
SOFTWARE: FastSEQ f
SEQ ID NO 10
LENGTH: 3792
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	igiticigatatgogogocacatticoaggacaagcoctitigititic tigicitogagtigaggacatgogocacaggaacggocagactitic [1][]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]	Db 2281 aacgttattcacaagttgtcaccactgctatcaagcgcaafgttcraagggtactg 2340 Oy 2341 gatcaagacatcgaactcctcgacatcgctatcaagcgcaaattctcacatcgcaa 2400   1341 gatcaagacatcgaactcctcgacatcccggagcaaattctcggtgctctcacatcgcaa 2400   1341 gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa 2400   1341 gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa 2400   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341   1341	2401 Cugloagecoacagagagugecagagagugeacaaallicecaallaata 2461 gitgiggtcaacatcgictcgagagugecctaccactagcctatggatugaaactggg 1111111111111111111111111111111111	0y 2581 tctagagacgaagctagaaactcggcaaactttgcagaaaqqctgggcttgc 2640	Oy 2761 ggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgcctggga 2820 [1][1][1][1][1][1][1][1][1][1][1][1][1][

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901 tttcgcatgtatcagaatgcgaaggttggcaaagtctttactgttgtcctt 960	1	1	### ### ### ### ### ### ### ### ### ##	### ### ### ### ### ### ### ### ### ##	1	1	1	1	1,	11/19/19/19/19/19/19/19/19/19/19/19/19/1	1   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   1990   199
841 tigiticicaactgagtactitigcatitacgcigctatcggcactggcctitiggaaaggt 900  901 titiogcatgatacagaaggtggcgaaggttggcgaaagtctttactgttgtcctt 960  901 titiogcatgtatcagaatggcgaaggttggcgaaggttggcaaagtctttactgttgtcctt 960  901 titiogcatgtatcagaatggcgaaggttggcgaaggttggcaaagtctttactgttgtcctt 960  902 2041 tgcatcctaaccatgttctaaggttggcgccttcaaggttcaagtcgttac 1020  961 tccgtcaaccttagcaacgtccatctcaatggttggcgccttcaggtcgttac 1020	1	1	###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   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Pred. No. 0;
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US-09-351-224-9
Sequence 9, Application US/09351224
Sequence 9, Application US/09351224
GENERAL INFORMATION:
APPLICANT: DUVICK, Jon
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/351,224
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ IO NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Exophiala spinifera
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Best Local Similarity 96.1%;
Matches 3658; Conservative
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οy	1615	ctaccagcgccttgacccgaaggcggag 167
qq	1638	cggatcccaagatcctgttactcgatgaagctaccagcgccttgacccgaaggcgga
Oy	1675	cottgaaccgagtgtccaaagaccgcactactt
qq	1698	aagtggtccaggaggccttgaaccgagtgtccaaagaccgcactactttggtcattgcc 17
0y	1735	acaaactagccactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaaatc 17
ф	1758	caaactagccactgtcatacgactcactattagggcgaattgggccctctagatgcat 18
Qy	1795	gagcaaggcacacacacgaattgatcgattcggctgtcattacgccgcac 184
q	1818	ctcgagcggccgccagtgtgacgaattgatgcagaattcggcttgtcattacgccgcac
Oy	1850	cggggctgacgaacaacaagaacatgagaagacctgcacg 190
qq	1878	ggtgcgtgcacaggacctcggggctgacgaacaagaagaacatgagaagaccctgcac
03	1910	aaaaggcagcacgagaagctgctggtgaacgaccggcacttgagcgcactcacaccactg 1969
QQ	1938	aaaygcagcacgagaagctgctggtgaacgaccggcacttgagcgcactcacaccactg 199
Qy	1970	gagacctggagaagcggaaggtgccggtcg
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<b>q</b> O	2058	getectaaaatgeateetaateatgttetaegaacaaaaaaatetetaetggtgettet 211
ογ	2090	ttgtcaacaataacggttctgatatgcgcggccacatttccaggacaagccttttgt 21
qq	2118	gttgtcaacaatagcggttctgatatgcgcggccacatttccaggacaagccctttgt 217
oy	2150	agattgotcactgtcttcgagttgagtggtcatgcggcacaggaacgggcagact 22
Q	2178	ttcgagattgctcactgtcttcgagttgagttgtgtgtcatgcggcacaggaacgggcagact 223
Qy	2210	ttctgatgttctttgtcgtggctctaggaaatctagtaggatatttcacgattg 22
qq	2238	ttatagicigaigticitigicgiggiggiggiggiggigggatatticacgaitg 229
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qq	2298	ciggacatgcaacgiigtiicacaagiigicacccaicgciatigagccgaaaigiicc 235
δλ	2330	aacgagtactggatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctc 2389

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gecaatgetttggattttgteatetetttaceagaaggetttgaaaegeettgeggetea
                  DB 17; Length 3999;
                                                                                                                                                                                                                           Methods for Fumonisin
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                                                                                                                                                                                        APPLICANT: DAVICK, Jon
APPLICANT: DAVICK, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Crasta, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Detoxification
FILE REPERPORE: 5719-111
CURRENT FILICATION NUMBER: US/09/351,224E
CURRENT FILION DAVIS: 1999-07-12
SOFTWARE: FastSEO for Windows Version 4.0
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Pred. No. 0;
4; Mismatches
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                                                                                                                                            ; Sequence 9, Application US/09351224E; GENERAL INFORMATION:
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ORGANISM: Exophiala spinifera
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Best Local Similarity 96.1
Matches 3558; Conservative
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LOCATION: (0)...(0)
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ORGANISM: Exophiala spinifera
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RESULT 14
US-005-677-488-9
US-005-677-488-9
Sequence 9, Application US/09677488
GENERAL INFORMATION:
APPLICANT: DUVICK, JON
TITLE OF INVENTION:
COMPOSITION COMPOSITIONS and Methods for Fummonisin Detoxification
FILE REFERENCE: 35718/204100 (5718-111A )
CURRENT APPLICATION NUMBER: US/09/677,488
CURRENT FILING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR PLIING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SSPTWARE: Patentin Ver. 2.0
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Pred. No. 0;
4; Mismatches 126; Indels
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                                            TYPE: DNA
ORGANISM: Exophiala spinifera
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Best Local Similarity 96.1%;
Matches 3658; Conservative
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                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature

: LOCATION: (0)...(0)

: OTHER INFORMATION: p-glycoprotein, with introns

US-09-677-488A-9
                                                                   APPLICANT: Duvick, Jon
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Craste, Otto
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Compositions and Methods:
TITLE OF INVENTION: Composition and Methods:
TITLE OF INVENTION: Composition and Methods:
TITLE OF INVENTION: CASE JOHNORS: 10-02
SEQ ID NOS: 11
SEQ ID NO 9-00
SEQ ID NO 9-00
                                                                                                                         Methods
tttggcacaatctttagaccaagcatga 3823
                                                 ; Sequence 9, Application US/09677488A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                   ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 3558;
                             RESULT 15
US-09-677-488A-9
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Search completed: April 27, 2002, 01:38:22 Job time: 22266 sec

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Sequence 230, Appl
Sequence 21, Appli
Sequence 1, Appli
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US-08-996-644-1

US-08-996-644-1

US-08-996-644-1

Sequence 1, Application US/08996644

Patent No. 594524

GENERAL INFORMATION:

APPLICANT: Skatrud, Paul L.

APPLICANT: Radard, Maarten

TITLE OF INVENTION: Maltiple Drug Resistance Gene atrC of

TITLE OF INVENTION: Aspergillus Nidulans

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDERSS:

MUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDERSS:

ADDERSSEE: Eli Lilly and Company

STREET: Indianapolis

COUNTY: U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3927;
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ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: floopy disk
MEDIUM TYPE: floopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/996,644
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
RECISTRATION NUMBER: 39,872
REFERENDE/COCKET UNMBER: 39,872
TELECHONE: 317-276-3334
TELECAN: AND TOWNER: AND TELECAN: AND TELEC
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Pred. No. 1.2e-228;
3 US-09-096-867-2
4 US-08-968-259-79
4 US-08-103-840A-230
4 US-09-103-840A-1
3 US-08-772-270A-14
3 US-08-772-270A-1
2 US-08-72-270A-1
2 US-09-103-840A-1
4 US-09-103-840A-1
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Oy 583	3 tggaagctagctttaatcaccatgtccgtcatccctgccatttcctggtcaccggcatc 642
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Qy 643	3 tgcatagcaattgatgccgctcaggaggccaggatcaccaggatctactcacgcgccgct 702
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Qy 763 Db 889	3 aaaatggtcgaaaaatatgatgtcttttgcagcaagcacaccaagaaggaag
Oy 823	3 tegecaaataatggsgtettgtteteaaetgagtaettttgeatttaegetgetategea 882
Ob 949	
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Db 1009	
Oy 943 Db 1069	3 gtctttactgttgtcctttccgtcaccttagcagccacgtccatctcaatgcttgcgcct 1002
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Db 1129	
Oy 1062	2 caaacccacgcagctcgaccctctcgaccttctggaaagcagccagagggctgcctagg 1121
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tgacccgaaggcggagaaagtggtccaggaggccttgaaccgagtgtccaaagaccgcac 1718 ttacgccgcactggtgcgtgcacaggacctcggggctgacgaacaacaagaacatgagaa 1898 AAATGAGGAGGTGAAGGCGAAGATGTCGCTCTCCTGGAGGTCACCGAAACAGCAGTAAC 2087 tototaciggigoticitigitgicaacaataacggittotgataigcgcggccacatitcc 2132 aggacaagcccttttgttttcgagattgctcactgtcttcgagttgagtggtcatgcggc 2192 CGGCCAAGCTATCTTGATGTCTCGCGTTGTCGAGGTCTTCAGGCTTCGGGAGACGCTAT 2327 1182 tcgagatttcaacttgacaattccagctggcaagacggcctcgtcggtgcatcagg 1308 CGATAACTICAGTCTCAAGGTCCCAGGGGAAAGGTGACTGCCCTGGTAGGGCAATCTGG CGCCTCGTCGGGACGCCGTGGGAATGCCTCTCGGGAAGAGAGATGGAACGGTCTCA gactgaagttggcgagcgagccggagccttgagtggaggtcaacgacaacgaattgcaat tegeetegtteaacaggaacetgtgttgtttegtggcacaatettecagaacattgecaa 1788 TGATCCGCATCCAGAGGATTGTTCAGAAGGCTCTGGACAAAGCAGCTGAGGGGCGCAC 1968 CTATGCCGGTCTGGTCAAAATCCAGAACCTGGCAGTGAATGCTTCAGCACATGACAATGT gaccetgeacgaaaaggeaggeacgagaaget....getggtgaacgaecggeacttga gegeacteacactgecacateteaagetggagacetggaggaaggeggtgeeggt tagoggcaaaagcacaatggtcggcttacttgaacggtggtatctgcccagttcgggggag cggtttcatggatgagcaacgag...atctgcctcgcgaaaaaaaatggagcttgtgca asasactigcasagccagcasiggcgacgigticatiasigagcticcgaacggitatgs 1668 TACGCTGATCGGCGAACGGGGTGGTCTGCTTTCTGGAGGCCAGAAGCAGCGGGTTGCGAT CCGCTACCCAACCTCCATCCGCGGTCGAATGAACTCCATAAAGGACCGCGACGATTATGA cgggactttggggctactcgctcctaaaatgcatcctaatcatgttctacgaacaaaaaa ACTGAAATGGGCCTATCTCGTCGTGCTACTGGGGTGTCTTGGTGGTTGCGCCATGTACCC a δ qq g ò

	RESULT 2  1. Sequence 1. Application US/0935252  1. APPLICANT: Startud, Paul L. APPLICANT: Startud, Paul L. APPLICANT: Startud, Paul L. APPLICANT: Startud, Paul L. APPLICANT: Ge Maard, Maarteen  1. TITLE OF INVENTION: Multiple Drug Resistance Gene atrC of TITLE OF INVENTION: Mapergillus Middlans  1. CORRESPONDENCE: 3  1. CORRESPONDENCE ADDRESS: 3  1. CORRESPONDENCE ADDRESS: 3  1. COUNTRY: Indianapolis  1. COUNTRY: Indianapolis  1. COMPUTER READABLE FORM: WE COMPATION: MULTIPLE PARTION: PAPLICATION NAMES: US/09/352,552  1. CORPARE: Patentin Release #1.0, Version #1.30  1. CORPUTER: IPM PORMYION: MARSHING SYSTEM: NAME: Webster, Indomas D. FILING DATE: TILNG DATE: TILNG DATE: TILNG DATE: TELEBONE: 39,872  1. RELEBONE: 317-276-334  1. RELEBONE: 317-276-276  1. RELEBONE: 317-276-276  1. RELEBONE: STARANDENDENS: SINGLE
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1.3924
US-09-32-52-1
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 Length 3927;
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 Score 723.6; DB 3;
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1; Mismatches 1745;
 19.1%;
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Patent No. 5945324

GENERAL INPORATION:
APPLICANT: Skatud, Paul L.
APPLICANT: Ge Waard, Marten
TITLE OF INVENTION: Appergillus Nidulans
INUMER OF SQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
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MEDIUM TYPE: Floppy
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.larity 38.5%; Pred. No. 3.5e-228;
Conservative 502; Mismatches 1744;
       TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-276-3334
TELEPHONE: 317-276-276-334
TELEPHONE: 317-276-276-334
TELEPHONE: 317-276-276-335
TENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERIZINGS:
LENGTH: 3924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: Innan
REFERENCE/DOCKET NUMBER:
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Matches 1426; Conserv
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US-08-996-644-3
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APPLICANT: Ge Waard, Maarten
TITLE OF INVENTION: Multiple Drug Resistance Gene atrC ritle OF INVENTION: Multiple Drug Resistance Gene atrC ritle OF INVENTION: Aspergillus Nidulans
NUMBER OF SEQUENCES: Aspergillus Nidulans
ADDRESSE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09352552 Patent No. 6060264
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.larity 38.5%; Pred, No. 3.5e-228;
Conservative 502; Mismatches 1744;
APPLICATION NUMBER: US/09/352,555
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/996,644
FILING DATE:
ATTONNEY,FAGENT 1NDORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-117f
TELECOMUNICATION INFORMATION:
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TELECOMUNICATION INFORMATION:
TELECOMUNICATION ON S:
SEDOENCE CHARACTERISTICS:
LENGTH: 3924 base pairs
TYPE: nuclel acid
STRANDEDNESS: SIDGLE
TOPOLOGY: linear
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Fatent No. 5928898
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Statted, Paul L.
APPLICANT: Deery, Robert B.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
TITLE OF ENVENTION: Aspergillus Nidulans
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
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                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,545
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                       Lilly Corporate Center
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 3, Application US/08996545
Sequence 3, Application US/08996545
Settent No. 592898
GENERAL INFORMATION:
APPLICANT: Skatrud, Paul L.
APPLICANT: Peery, Robert B.
APPLICANT: Peery, Robert B.
APPLICANT: Andrade, Alan C.
APPLICANT: Andrade, Alan C.
ATTILE OF INVENTION: Multiple Drug Resistance Gene at TITLE OF INVENTION: Aspergillus Midulans
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12.8%; Score 487; DB 2; Length 400
Best Local Similarity 35.6%; Pred No. 2.96-150;
Matches 1267; Conservative 464; Mismatches 1760; Indela
                                                                                     ZIP: 46285.

ZIP: 46285.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,545
FILING DATE:
                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEBDER: 39,872
REGISTRATION NUMBER: 39,872
RETERENCE/DOCKET NUMBER: x-117
TELECOMMUNICATION 17-276-3334
TELECOMMUNICATION 17-276-3334
INFORMATION FOR SEG ID NO: SEQUENCE CHARATERISTICS:
LENGTH: 4002 base pairs
TYPE: DUCLEIC acid
STRANBEDRES: single
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Ell Lilly and Compa
STREET: Lilly Corporate Center
CITY: Indianapolis
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MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
                                                                      Indiana
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US-08-996-545-3
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grecaageageageceagtatttggettactecaegagttttaccaaggeteggtegget
                             3116 CUCAAUCCGCGGGCACCGUCUUUUCCUUUGCACCAGA-CAUGGGCAAGGCGAAGAAUGCG
                                                                                                        GCCGCCGAAUUCCGACGACGACGAAGCCACAAAUUGAUAACGGUCUGAAGAG
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Patent No. 6228615
GENERAL INFORMATION:
APPLICANT: SKATUHG, Paul L.
APPLICANT: Ge Waard, Maarten A.
APPLICANT: Peery, Robert B.
APPLICANT: Andrade, Alan C.
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US-09-328-320-1
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                                                                             682 aggatetacteacgegeegetgteetegeagaagaagtettateateateeggaeagte
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Pred. No. 2.9e-150;
0; Mismatches 1760; Indels 68; Gaps
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                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,320
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Córporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,545
                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFRENCE/DOCKT NUMBER: X-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-3763
INFORMATION FOR SED ID NO:
SEQUENCE CHARATERISTICS:
LENGTH: 4002 base pairs
TYPE: NUCLEIC acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.8%;
                                                                                       COUNTER READABLE FORM:
COMPUTER READABLE FORM:
THE READABLE FORM:
THE READABLE FORM:
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Best Local Similarity 48.6
Matches 1731; Conservative
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..4002
US-09-328-320-1
                                                                          Indiana
                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                      COUNTRY:
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Db 2996 CGCAGGCACTTGTTTCTTCTGCGTTGCG  Qy 2845 cttcaggtgagtacgacacaactcaattt	3116	3175	3025	3295	3355	3415	3475	3325	3384 3595	3444	3714	3564	3834	Oy 3684 tgtgtttgccaacggggagaatcgccgaaa 	Oy 3744 aggaagatattacgagatg 3762 	RESULT 8     US-09-328-320-3     Sequence 3, Application US/09328320     Patent No. 6228615     GENERAL INFORMATION:
1759 getggcaacatcgcagtcatttcccaggggaaaatcgtcgagcaaggcacacaca	1981 THGSTTGACCCCGGGGGCCTTATCGCAACTTGTGGGGGCTCAACGTATCAATGAACGG 2040 1862aggacctcggggctgacgacaacaagaacatgagaagac 1902 2041 AAGGAACGTGAGGCGCAGGTGAGGGATGACGAAATTGAGAAATTGC 2100	geageaggagagtgetgetgetgeacgaccggcacttgagcgcactcac	1963 accactgccacatctcaagctggagacctggagaggcggaaggtgccggtcggg 2016 111   1   1   1   1   1   1   1   1   1	2017 actttgggctactcgctcctaaaatgcatcctaatcatgttctacgaacaa 2067	2068 aaaaatctctactggtgcttcttgttgtcaacaataacggttctgatatgcgcggccaca 2127   1   1   1   1   1   1   1   2281 ArccGTaCATGGTCTCTCTCTTCTCAGTTGTTGTGGTGGCCAACCCACG 2340	2128 tttccaggacaagccttttgttttcgagattgctcactgtcttcgagttgagtggtcat 2187 	2188 goggcacaggaacgggcagacttttatattctgatgttctttgtcgtggctctaggaaat 2247	2248 ctagtaggatatttcacgattggctggacatgcaacgttatttcacaagttgtcacccat 2307   1   1   1   1   1   1   1   1   1	2308 cgctatcaagccgcaatgttccaacgagtactggatcaagacatcgaactcctcgacatc 2367 	2368 ccggagcaaatttctggtgctctcacatcgcaactgtcagctctaccacacagtgcaa 2427 	2428 gagttgatatcagcaaattttctcatttatatcgttgtcggtcaacatcgtctcgagc 2485   1   1   1   1   1   1   1   1   1	2486 agtgctctaccactagcctatggatggaaactgggcctggtggttgtttggtgcactt 2545 	2546 ccaccctgcttttggctggctacctcagaattcgtctagaagacgaagctagaagccgga 2605   1   1   1   1   1   1   1   1   1	2606 aactoggcaaactttgcagaaagtgctgggcttgcaagcgaagcagttacogcgatccgg 2665	2666 accgleteatetttgaetetegaaggeeatgtieteeaaeagtaeteggaeatgttgage 2725 	2726 aaggtettget 
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APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
APPLICANT: de Waard, Maarten A.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of
TITLE OF SEQUENCE: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 1
CORRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapoils
COUNTRY: U.S.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-COMPATIBLE
OPERATING SYSTEM: PC-COMPATIBLE
OPERATION NUMBER: US/09/328,320
CLASSIFICATION NUMBER: US/09/328,320
CLASSIFICATION NUMBER: 08/996,545
FILING APPLICATION NUMBER: 08/996,545
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                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D, 872
REGISTRATION NUMBER: 39,872
REFERENCE/COCKET NUMBER: X-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Sequence 1, Application US/08612734B
Patent No. 5914246
GENERAL INFORMATION:
APPLICANT: Skatrud, Paul L.
APPLICANT: Skatrud, Paul L.
APPLICANT: Skatrud, Paul L.
APPLICANT: TITLE OF INVENTION: Multiple Drug Resistance Gene of TITLE OF INVENTION: Aspergillus Fumigatus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/612,734B
FILING DATE: 08-WAR-1996
CLASSIFICATION: 435
ATCARSIFICATION: Anne I.
REGISTRATION: Anne I.
REGISTRATION: NUMBER: X-9681
FELECOMMUNICATION INDERER: X-9681
TELECOMMUNICATION INDERER: X-9681
TELEGRATION FOR SEQ ID NO: 1:
SEGUENCE CHRARACTERISTICS:
LENGTH: 4047 base pairs
WVDFWATTON FOR SEQ ID NO: 1:
SEGUENCE CHRARACTERISTICS:
LENGTH: 4047 base pairs
                                                                                                                    of
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Pred. No. 3.4e-138;
0; Mismatches 1869;
                                                                                                                                                              STREE: Eli Lilly and Company STREE: Lilly Corporate Center, DC1501 CITY: Indianapolis STATE: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
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Best Local Similarity 47.5%;
Matches 1769; Conservative C
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STRANDEDNESS: single
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; LOCATION: 1..4
US-08-612-734B-1
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                                                                                                                                                                                                                                               PATENT NO. 5914246
GENERAL INFORMATION:
APPLICANT: Peery, Robert B.
APPLICANT: Statud, Paul L.
APPLICANT: Matthew B.
TITLE OF INVENTION: APPETGILLUS Fumigatus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
FILE OF THE OF THE OF THE OFFICE ADDRESS:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PALENT Release #1.0, Version #1.30
CUBRENT APPLICATION DATE:
FILING DATE: 08 -MAR1996
CLASSITCATION NUMBER: US/08/612,734B
FILING DATE: 08 -MAR1996
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CLASQ'A Annel:
NEGISTATION NUMBER: 32.976
REFERENCE/DOCKET NUMBER: 32.976
REFERENCE/DOCKET NUMBER: 32.976
TELLEPAX: 617-354-4043
INFORMATION FELEPHON: 617-354-4043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4800 base pairs
TWEEN.
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1.4e-110;
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46.7%; Pred. No. 1.4e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                 Sequence 3, Application US/08612734B Patent No. 5914246
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STRANDEDNESS: double
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US-08-612-734B-3
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Db 3087 CTGGTTGGTGTTCCAATCTTTGGCATGGGCTTCCTCAGATTCTAC 3143  Qy 2582 ctagagacgaagctggaaactcggcaaactttgcagaaagtgctgggcttgca 2641  Db 3144 ATGCTTGCTCAATTCCAGCAACGATCGCTACGAAGGGTGTGCGAGCTATGCT 3203  Qy 2642 agcgaagcagttaccgggatcggtctcatctttgactctcgaaggccatgttct 2701  Db 3144 ATGCTTGCTCAATTCCAGCAACGATCGCTACGAAGGGTGTGCGAGCTATGCT 3203  Qy 2642 agcgaagcagttaccgggatcggtctcatctttgactctcgaaggccatgttct 2701  Db 3204 TGCGAAGCCAGTCAGCATCAGCATCACTCACTGCGAACAAATTGTTGG 3263  Qy 2702 caacagtactcggacatgttgagcaaggtcttgcaagatcatccaaagcttttggtttg 2761  Db 3264 GGCGTTTACCACGACCAGCT-ACAAAAAACAGGGAAGAAGTTGATCTGAGTGTGA 3321	Oy 2762 gacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgccttgggat 2821 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	3502 ACATGGGTAAGGCAAGAATGCCGCTGCTCAATTCAAGAAACTCTTCGACAGCGAA 3002 ccatccgggaaacggaaacaagaaaaaggcccagtgggtgg	As a sea of state and a sea of	Qy         3421 ttgtcatctctttaccagaag           bb         3982 TCGTANGTCACTCCGTAGGTTACTGCCTGGCTGCTTCATGCCTGCGGGTTTT 4041           Cy         3442
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                                                   4162 CCTTCTTCTGGATGAAGCCACATCTGCTTTGACTCCGAATCTGAGAAAGTCGTACAAGC
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                                                                                                                                                       APPLICANT: Search, Robert B.
APPLICANT: Skartud, Paul L.
TITLE OF INVENTION: MULTIPLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: ASPERGILLUS FLAVUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: USEN
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATE:
FILING DATE:
FLING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: Plant, Thomas G.
REGISTRATION NUMBER: 35784
RELEEPHONE: 317-276-2459
TELEFRAN: 317-276-2459
TELEFRAN: 317-276-2459
TELEFRAN: 317-277-1917
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRANCTH: 3924 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                    Sequence 1, Application US/08395246C; Patent No. 5773214
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-395-246C-1
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US-08-395-246C-1
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1336 GGGGGACCATTATGCTCGACGCCACGATATCCAGACATGAATCTCCGATGCTGCGA 1395	1354 agocgcattcgcctcgttcaacaggaacctgttgtttcgttggcacaatcttccagaac 1413	1414 attgccaacggtttcatggatgatgacacgagatctgcctcgcgaaaaacaaatggag	1471 cttgtgcaaaagcttgcaaagccagcaatggcgacgtgttcattaatgagcttccgaac 1530	1531 ggttatgagactgaagt {{{	1591 attgcaatcgcacgaagtatcatatcggatcccaagatcctgttactcgatgaagctacc	1651 agogocottgacocgaaggogagaaagtggtocaggaggocttgaacogagtgtocaaa 1710 	1711 gaccgcactactttggt                       GTAGAACGACTATTGT	1771 gcagtcatttcccaggg                1810 ATTGTTCTTGCCAATGG	1831 ggctgtcattacgccgc   1831 gctgtcattacgccgc   1   1   1   1   1   1   1   1   1	1865acctcggggctgacgaacaacaagaacatgagaagacctgcac 1908	1909 gaaaaggcagcacgagaagctgctggtgaacgaccggcacttgagcgcactcacaccact	1969 gccacatctcaagctgg 	1990 ctggagaagcggaaggtgcgggactttgggctactcgctcctaaaatgcatccta 2049	2050 atcatgttctacgaacaaaaatctctactggtgcttcttgttgtcaacaataacggtt	2110 ctgatatgcgcggccac           2230 ATACTGGCAGGGGAT	2170 ttcgagttgagtggtcatgcggcacaggaacgggcagactttatattctg 2220	2221 atgitetitgiogigotetaggaaatetagiaggataiiteacgaiiggeiggacaige 2280	
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1411 AAGCTTTTCGCAACTATCGACCGTGTACCCGCCATTGATTCGCCAGGAAGGTTTC 1470
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                                     Indels
   Best Local Similarity 46.5%; Pred. No. 2.9e-105; Matches 1661; Conservative 1; Mismatches 1829;
Best Local Similarity
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COMBUTER: IBM PC Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,521
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Fatent No. 5786463
Fatent No. 578646
Fatent No. 57864
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAMLILOD, AMY E
REDISTRATION UNDER: 33.894
REFERENCE/DOCKET NUMBER: 33.894
REFERENCE/DOCKET NUMBER: 42.96
TELECOMMUNICATION INFORMATION:
TELEPRAS: 317.276-3169
TELEFAX: 317.276-1294
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 42.24 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; LOCATION;
US-08-612-521-1
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tetttaccagaaggetttgaaacgeettgeggetcaacgagggatgeagtteteeggegg
                 POLYNUCLEOTIDE AND POLYPEPTIDE
SEQUENCES ENCODING RAT MDRIB2 AND
SCREENING METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,513
FILING DATE: 22-JUL-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: SmithKilne Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
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Patent No. 6025160
GENERAL INFORMATION:
APPLICANT: Brun, Kimberly
APPLICANT: Chenery, Richard
APPLICANT: Chenery, Richard
APPLICANT: Field, John
APPLICANT: Field, John
APPLICANT: Field, John
TITLE OF INVENTION: SEQUENCES ENCO;
TITLE OF INVENTION: SEQUENCES ENCO;
TITLE OF INVENTION: SEQUENCES ENCO;
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
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; MOLECULE TYPE:
US-09-120-513-1
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Similarity 44.9%; Pred. No. 1.2e-83;
44; Conservative 2; Mismatches 1832;
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APPLICANT: Kimberly Anne Brun
APPLICANT: Albard James Chenery
APPLICANT: Harma Ellanes
APPLICANT: Harma Ellanes
APPLICANT: John Anthony Feild
APPLICANT: John Anthony Feild
TITLE OF INVENTION: ENCODING RAT MORIB2 AND SCREENING METHODS THEREOF
TITLE OF INVENTION: ENCODING RAT MORIB2 AND SCREENING METHODS THEREOF
CURRENT APPLICATION NUMBER: US/09/450,105
CURRENT FILING DATE: 1999-11-29
EARLIER APPLICATION NUMBER: 09/120,513
EARLIER FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                              3633 aatagcagtggcgcaccgactttccactattcggaatgttgatgttatttttgtgtttgc 3692
                                                               GAACGCCCAGGTCAAGGAGCACCGCCACCAGCAGCTGCTGCCCCAGAAAGGCATCTA 3816
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Similarity 44.9%; Pred. No. 1.2e-83;
44; Conservative 2; Mismatches 1932;
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING 'SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 270.2; DB 1;
Similarity 44.9%; Pred. No. 2.1e-78;
17; Conservative 1; Mismatches 1824;
                        Drive, Suite 300
                                                                                                                                                                                                SOFTWARE: Patentin relection CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,471
FILING DATE: 13-JAN-1994
CLASSIPICATION: 424
PRIOR APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELETHER AG 19-792-8477
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CARROCTERISTICS:
LENGTH: 4646 base pairs
TTPE: nucleic acid
TTPE: nucleic acid
TTPE: nucleic acid
ADDRESSEE: Thomas Fitting
STREET: 12526 High Bluff |
CITY: San Diego
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425..4267
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MOLECULE TYPE: CDN
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                                                        STATE: CA
COUNTRY: USI
ZIP: 92130
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; LOCATION:
US-08-181-471-2
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Matches 1537;
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Page 31

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2308 GCAGACAGCAGGAAATGAAGTTG	1915 gcagcacgagaagctgctggtga 	1975 totcaagctggagacctg 	2030 cgctcctaaaatgcatcc                     2488 GGATGAAGTATACCTCCAGTTT	2079 ctggtgcttcttgttgtcaacaa                 2548 GCCTTATTTGTTGTTGTTGTTAT	2139 agccttttgttttcgagattgc 	2199 acgggcagactttatattctga               2668 ACGACAGAATAGTAACTTGTTTT	2253 aggatattcacgattggctgga             2728 TACATTTTCCTTCAGGGTTTCA	2313 tcaagccgcaatgttccaacgag 	2373 gcaaatttctggtgctctcacat                 2848 AAACACCACTGGAGCATTGACTA	2433 gatatcagcaaattttctcat 	2491 tctaccactagcctatggatgga 	2551 cctgcttttggctggctacctca 	2611 ggcaaactttgcagaaagtgctg                 3085 GaaaGactaGaaGGTGCTGGGA	2671 ctcatcttgactctcgaaggcc 	2731 cttgctaagatcatccaaagctt 	2791 tcgatggagtttttggctattgc 	2851 gtgagtacgacacaactcaattt         3323 AAACTCATGAGCTTTGAGGATGT	2911 gcagcagcccagtatttggctta                3383 GCGTGGGGCAAGTCAGTTCATT
qq	oy do	Oy Op	yo da	Qy Qp	λ q q	o o	Oy Db	oy op	Qy	Oy	Oy Db	Qy Dp	Oy Db	oy Op	Qy Dp	oy Dp	oy Db	Qy Dp

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3683 TACGACCCCTTGGCAGGGAAAGTGCTGCTTGATGCCAAAGAAATAAAGCGACTGAATGTT 3742
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2971 tatatoctotggotgogacattgaagoogaccatcogogaaaoggaagaagaaaa 3030
             3091 cgtgattcggctcgagttctccgggggtttccatgacaatcgagccaggacaatttgta 3150
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4222 CTATT 4226
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Search completed: April 27, 2002, 01:39:27 Job time: 22456 sec

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Run on:

Aspergillus flavus cDNA encoding a mu P. chrysogenum ABC P. chrysogenum ABC P. chrysogenum ABC Prosophila melanog H. contortus PGP-A Murine multidrug resil P. chrysogenum ABC P. chrysogenum ABC Human APC P. chrysogenum ABC Human APC P. chrysogenum ABC Human APC Pinding Human APC Pinding Human APC Pinding Human APC Pulding Fat mdribz (multidrug re Rat mdribz (multidrug re Rat mdribz (multidrug prospercien) Dog P-glycoprotein Dog

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Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permease; p-dyrooprotein; fumonisin esterase; detxxification; mycotoxin; animal feed; himan feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag* a
/product= "E. spinifera p-glycoprotein"
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                                             AAFB3380

ABL 43381

AAV 69392

AAV 69392

AAZ 6933

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AAZ 6933

AAZ 6934

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AAZ 6933

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Result

Sequence of human

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The patent discloses novel polynucleotides encoding Exophiala spinifera funchial degradative or transport enzymes such as flavin annonoxygenase, funchial degradative or transport enzymes such as flavin annonoxygenase, and projection. A funchisin esterase enzyme with at least one funchisin degradative enzyme is useful for enzyme with at least one funchisin or a structurally related mycrotxin present in harvested grain, on application to a plant or to harvested grain or a structurally related mycrotxin present in harvested grain, on application to a plant or to be used as animal curvention are useful as probes and primers. They can be introduced invention are useful as probes and primers. They can be introduced for into micropaphisms that multiply on plants to deliver enzymes to potential target crops. The genes encoding the degrading enzymes are introduced to the environment, plants or animals for reducing the pathogenicity of a fungus producing funchish. The genes of the pathogenicity of a fungus producing funchish. The genes of the pathogenicity of a fungus producing funchish. The grees of the can be used alone or in combination to engineer microbes or other corpusations to maintain the present DNA sequence is the p-glycoprotein coding sequence from Exophiala spinifera.
                                                                                                                      Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food consumption
                       QR;
                       Crasta
                    ò
                    Folkerts
                                                                                                                                                                                                                                                 Claim 1b; Page 75-77; 90pp; English
                    Gilliam J,
                    ٦,
                                                                2001-147345/15
                    Maddox
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Sequence 3792 BP; 939 A; 983 C; 928 G; 940 T; 2 other;

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qa	2761	gatgittiggitticacitgicacagicgaiggagittitggciaitgccciggga 282	50
δλ		88	
QQ	2821	ttigtattgcagtcgataattggcttcaggtgagtacgacacaactcaattttatatca 288	
ΟŸ	2881	cttcgtgggggttttgtttgccggtccaagcagcccagtatttggcttactccacg 2940	
qq	2881	ticgiggggggttttgtttgccggtccaagcagcagcagtatttggcttactccacg 294	
OY	2941	8	
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qa	3241	cacacgagaatattgcagaaatgtcgccgcgttgtaccgcggccatatgtctttggtc 330	
OY	3301	ggaacccacactttaccaaggctccgttcgcgagaatgtgacgttggccctcgaa 336	
qa	3301	aacaggaacccacactttaccaaggctccgttcgcgagaatgtgacgttggccctcgaa 336	
δy	3361	ccgaattatcagaagagctttgtcaaggacgccttcccgcaaggccaatgctttggatt 342	C
q	3361	cgaattatcagaagagctttgtcaaggacgccttcccgcaaggccaatgctttggatt 342	
Qy	3421	tgtcatctctttaccagaaggctttgaaacgccttgcggctcaacgagggatgcagttc 348	
q	3421	gtcatctctttaccagaaggctttgaaacgccttgcggctcaacgagggatgcagttc 348	
03	3481	ggcgggcaacgacagcggatcgccatcgcaagagcattgattcgaaatccaaagctg 354	4
qo	3481	cggcgggcaacgacagcggatcgccatcgcaagagcattgattcgaaatccaaagctg 354	
Οŷ	3541	ctacttgacgaagcgacgtcagcctcgacacgcaatcggaacgtctggttcaagct 360	
qa	3541	gctacttgacgaagcgacgtcagccttcgacacgcaatcggaacgtctggttcaagct 360	
Οy	3601	99	Ō
qu	3601	coctogatgaggcatccacgagccgaacgacaatagcagtggcgcaccgacttccact 366	
Ογ	3661	ā	ā
QO	3661	ttoggaatgitgatgitattitigigittigccaacgggagaatogoogaaacgggcact 372	
δ	~	78	æ
qq	3721	acgcggaactacaacgactgagaggaagatattacgagatgtgtttggcacaatcttta 378	

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The patent discloses novel polynucleotides encoding Exophiala spinifera
funonisin degradative or transport enzymes such as flavin monooxygenase,
aldehyde dehydrogenase, permease and p-djycoprotein. A fumonisin esterase
enzyme with at least one fumonisin degradative enzyme is useful for
aldehyde dehydrogenase, permease and p-djycoprotein. A fumonisin esterase
enzyme with at least one fumonisin of a structurally related mycotoxin present in
harvested grain, on application to a plant or to harvested grain
during processing, or to processed grain that is to be used as animal
contains are useful as probes and primers. They can be introduced
or harvested grain as probes and primers. They can be introduced
into microorganisms that multiply on plants to deliver enzymes are
introduced via a vector into a microbial host and the transformed host
controlled to the environment, plants or animals for reducing the
pathogenicity of a fungus producing fumonish. The genes of the
pathogenicity of a fungus producing fumonish. The genes of the
contains are fermented in a bacterial host and the resulting bacteria
is processed and used as a microbial spray. The nucleotide sequences
con be used alone or in combination to engineer microbes or other
corganisms to metabolise fumonish and resist its toxic effects.
The present sequence is a genomic DNA encoding Exophiala spinifera
                                                                                                                                                                                                                                                                               Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permease; pelyrooprotein; fumonisin esterase; detoxification; mycotoxin; animal feed; human feed; silage; transgenic animal; microbial spray; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food consumption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR;
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  Duvick JP, Maddox J,
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Gaps

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126; Indels

Score 3454.8; Pred. No. 0; 4; Mismatches

91.18; ilarity 96.18; Conservative

Query Match Best Local Similarity Matches 3658; Conserv

4;

DB 22; Length 3999;

us-09-882-694a-10\_1.rng

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The invention relates to a multiple drug resistance gene atrC of Aspergillus nidians. Host cells transformed with vectors comprising the atrC gene are used for the recombinant expression of atrC polypeptide. The atrC polymeteotide is used to produce nucleic acid molecules which are useful in disponsitic assays for detection of atrC polymeteotides. The atrC polypeptide may be used to identify agents which inhibit multiple drug resistance. These agents may be useful for the treatment of tingal diseases. New antifungal compounds may abe lateful for the treatment of the gene disruption or gene replacement strains of Aspergillus nidulans. The present sequence represents the CDNA encoding atrC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882
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                                                                                                                                                                                                                                        Length 3927;
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                                                                                                                                                                                                                                        19.1%; Score 723.6; DB 20;
larity 52.1%; Pred. No. 9e-217;
Conservative 1; Mismatches 1745;
                       New multiple drug resistance gene atrC
                                              Claim 2; Page 21-30; 45pp; English
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Matches 1929; Conserv
P-PSDB; AAY21815.
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gene disruption; ss.
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Llarity 38.5%; Pred. No. 2.5e-216;
Conservative 502; Mismatches 1744;
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                                                           (ELIL ) LILLY & CO ELI.
(UYWA-) UNIV WAGENINGEN AGRIC.
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Multiple drug resistance; atrD; fungal disease; antifungal;
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Pred. No. 4.2e-142;
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                                                                                       protein; AfuMDR1; activity; ss.
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The invention relates to a method for enhancing the secretion of beta-
lactam compounds from a micro-organism that comprises enhancing ABC dadenosine triphosphate (ATP)-binding cassette) transporter activity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC-transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents the genomic DNA sequence of the P. chrysogenum ABC transporter as10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins -
                                                                                                                                                                                                                                                                                                     Beta-lactam; micro-organism; ABC transporter; ATP-binding cassette; adenosine triphosphate-binding cassette; antibiotic; penicillin; cephalosporin; aal0; ds.
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Schuurs TA, Nieboer M, Westerlaken I;
                                                                                                                                                                                                                                                                 genomic DNA
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P-PSDB; AAB62495.
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11.5%; Score 436.6; DB 22; 47.0%; Pred. No. 5.7e-126; Elve 1; Mismatches 1890;

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The invention relates to a method for enhancing the secretion of beta-lactam compounds from a micro-organism that comprises enhancing ABC (adenosine triphosphate (ATP)-binding cassette) transporter activity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC-transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents the genomic DNA sequence of the P. chrysogenum ABC transporter aal0.
                                                                                                                                                     Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins
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The present sequence encodes the multiple drug resistance protein of Aspergilius funigatus, designated Afunbail. The specification describes a method whereby cultured transformed fungal cells are used to determine the multiple drug inhibition activity of a compound. The method is useful for providing nucleic acid molecules which encode multiple drug resistance proteins from Aspergillus fumigatus (Afu) which are useful for determining the WDR inhibition of a compound.
                                                                                                                                                                                                                                                                                                              Drug resistance gene from Aspergillus fumigatus useful for determining fungal multiple resistance inhibition activity
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            resistance protein; AfuMDR1; inhibition activity; ss.
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RESULT 10

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multiple drug resistance gene of Aspergillus flavus · used to ntify cpds. that inhibit fungal multiple drug resistance activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A cDNA clone (AAT35230) codes for a multiple drug resistance (MDR) protein (AAR99255), designated Afl-MDR1, of Aspergillus flavus. A cDNA library derived from mRNA of logarithmic phase mycella of A. flavus was screened with a probe obtd. by PCR amplification (see also AAT35231-32) of Afl-MDR1 genomic DNA present in pPSR-6 to obtain the full-length cDNA clone. The cDNA can be incorporated into a vector and utilised for prodn. of recombinant Afl-MDR1 in transformed host cells, pref. Saccharomyces cerevisiae, for use in identifying cpds. that inhibit fungal MDR activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3923 BP; 915 A; 1018 C; 1020 G; 970 T; 0 other;
                                                                                                             Multiple drug-resistance; MDR; Afl-MDR1; antifungal; ss
                                                                                  Aspergillus flavus multidrug resistance gene MDR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 16-22; 37pp; English.
ВР
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P-PSDB; AAR99255.
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AAT35230 standard;
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                               694 atgittictagcgactiggctttacatgitcatciggaatgitaciggcgagcicaacict 753
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transformed host cells, and
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                                                                                                                                                                                                                                                                                                     Multiple drug resistance protein; CneMDR1; identification; antifungal compound; resistance; ds.
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neoformans - also related vectors and
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P-PSDB; AAW62871.
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Best Local Similarity
Matches 1661; Conserv
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The invention relates to a method for enhancing the secretion of beta-lactam compounds from a micro-organism that comprises enhancing ABC (adenosine triphosphate (ATP)-binding cassette) transporter activity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC-transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents a partial cDNA sequence of the P. chrysogenum ABC transporter aal0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins -
                                                                    tgaggcatccacgagccgaacgacaatagcagtggcgcaccgacttccactattcggaa 3668
              Beta-lactam; micro-organism; ABC transporter; ATP-binding cassette; and triphosphate-binding cassette; antibiotic; penicillin;
                                                   tgttgatgttatttttgtgtttgccaacgggagagtcgccgaaacggggcactcacgcgga
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                                                                                                                                                                                                                                                                               chrysogenum ABC transporter aa10 partial cDNA
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Schuurs TA, Nieboer M,
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Score 344.8; DB 22; Length 3133; Pred. No. 2.7e-97;

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Query Match Best Local Similarity

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                                                                                            tttggtccaacaggaacccacatttaccaaggctccgttcgcgagaatgtgacgttggc 3353
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                                                                                                                                                                 Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins
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Les 843; Conservative 2; Mismatches 744; Indels 58;
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The invention relates to a method for enhancing the secretion of beta-lactam compounds from a micro-organism that comprises enhancing ABC (adenosine triphosphate (ATP)-binding cassette) transporter extrivity of the micro-organism. The method is used for enhancing the production and secretions of beta-lactam antibiotics like penicillin and cephalosporins. Manipulation of the ABC-transport protein system provides a means for enhancing beta-lactam secretion. The present sequence represents the genomic DNA sequence of the P. chrysogenum ABC transporter aal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enhancing secretion of beta-lactam compounds from a micro-organism by enhancing adenosine triphosphate-binding cassette transporter activity, useful for producing e.g. penicillin and cephalosporins -
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8.4%; Score 319.8; DB 22; Length 7744;
Best Local Similarity 51.2%; Pred. No. 3.8e-89;
Matches 843; Conservative 2; Mismatches 744; Indels 58;
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Schuurs TA, Nleboer M, Westerlaken I;
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99EP-0203685.
99EP-0203687.
99EP-0203689.
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99EP-0203692.
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P-PSDB; AAB62488.
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P-PSDB; ABB70072.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
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Search completed: April 27, 2002, 00:45:51 Job time: 19185 sec

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AF375879 Venturia
AF375879 Venturia
AF291822 Trichophy
U62934 Aspergillus
AR013812 Sequence
U62931 Aspergillus
U62929 Filobasidie
AF082072 Emericell
AL031307 S.pombe c
D10695 S.pombe pmd
M60041 C.griseus P
AF003908 Haemonchu
M59254 Chinese ham
M60040 C.griseus P
M55253 Chinese ham
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Exophiala spinifera

Exophiala spinifera

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes; Chaetothyriales; Herpotrichiellaceae; Exophiala.

(bases 1 to 3792)

Duvick,J.P., Maddox,J., Gilliam,J., Folkerts,O. and Crasta,O.R.

Compositions and methods for fumonisin detoxification
Patent: WO 0105980-A 10 25-JAN-2001;
Pioneer Hi-Bred International Inc. (US); Curagen Corporation (US)
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224 Synthetic
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M30697 Mouse multi
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AF071411 Aspergill
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| Db 961 TCCG | Oy 1021 caac<br>       <br>  Db 1021 CAAC                                                                                                                     | Oy 1081 cctc Db 1081 CCTC                                            | Qy 1141 ctgg<br>       <br>  Db 1141 CTGG | Oy 1201 attc | Oy 1261 gtcg<br>       <br>  Db 1261 GTCG | Qy 1321 gaac<br>       <br>  Db 1321 GAAC | Oy 1381 cctg                                     | Oy 1441 cgag:<br>                                                       | Qy 1501 ggcgi<br>       <br>  Db 1501 GGCG | Qy 1561 ggag<br>    <br>  Db 1561 GGAG | 1621 | Qy 1681 gtcc2<br>         <br>  Db 1681 GTCC2                         |                                                                          |                |                                                                        | 1921                                                                       | Oy 1981 gctgg<br>                                                                                                                                                    | Oy 2041 tgcat                                                             |
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| ORIGIN      | Query Match 100.0%; Score 3791.2; DB 6; Length 3792; Best Local Similarity 100.0%; Pred. No. 0; Matches 3792; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Qy 1 atggcagatgaatcggagaaacttcgaccaaaccaagatggcagtgagtcgtcctcacac 60 | = .                                       |              | 2 2 2                                     | 30                                        | Qy 301 ttcgtctacctctttattgggaagtttgtcctcacgtacgt | Oy 361 atttcagctatacgaaccactcgaactcttcgacgagtgttccttgaatgcaccttgcgg 420 | 4 4                                        |                                        | 0-0  | Oy 601 accatgiccgicatccctgccatticctggicaccggcatctgcatagcaattgaige 660 | Oy 661 gctcaggaggccaggatcaccaggatctacgcgcgcgctgtcctcgcagaagaagtc 720<br> | 721 t<br>721 T | y 781 gatgtcttttgcagcaagcaccaagaaggaagaagaaatcgccaaataatggsgtc 840<br> | Y 841 ttgttctcaactgagtacttttgcatttacgctgctatcgcactggccttttggaaaggt 900<br> | <ul> <li>901 tttcgcatgtatcagaatggcgaggttgccgacgttggcaaagtctttactgttgtcctt 960</li> <li>902 tTTCGCATGTATCAGAATGGCGAGGTTGCCGACGTTGGCAAGTCTTTACTGTTGTCTT 960</li> </ul> | 961 tccgtcaccttagcagccacgtccactccaatgcttgcgccttcaggttcagtcgtttac 1020<br> |
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| Oy<br>Db  | 2101         | ataacggttctgatatgcgcggccacatttccaggacaagccttttgttttcgagattg 2160<br>  |
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| QY<br>Db  | 2161<br>2161 | ctcactgtcttcgagttgagtggtcatgcggcacaggaacgggcagacttttatattctg 2220<br> |
| Qy<br>Dp  | 2221         | atgttetttgtegtggetetaggaaatetagtaggatattteaegattggetggaeatge 2280<br> |
| ζο,<br>Op | 2281         | aacgttatttcacaagttgtcacccatcgctatcaagccgcaatgttccaacgagtactg 2340<br> |
| oy<br>Ob  | 2341         | gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa 2400<br> |
| Oy<br>Dp  | 2401         | ctgtcagctctacccacgcagttgcaagagttgatatcagcaaattttctcatttatatc 2460<br> |
| Qy<br>Db  | 2461         | gttgtcggtcaacatcgtctcgagcagtgctctaccactagcctatggatgg                  |
| Qy<br>Db  | 2521<br>2521 | cctggtggttgtttggtgcacttccaccctgcttttggctgctacctcagaattcg 2580<br>     |
| Qy<br>Dp  | 2581<br>2581 | tctagagacgaagctagaagccggaaactcggcaaactttgcagaaagtgctgggcttgc 2640<br> |
| oy<br>Og  | 2641         | aagegaagcagttacegegateeggaeegteteatetttgaetetegaaggeeatgttet 2700<br> |
| o d       | 2701         | ccaacagtactcggacatgttgagcaaggtcttgctaagatcatccaaagcttttggttt 2760<br> |
| Oy<br>Dp  | 2761<br>2761 | ggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgcctggga 2820<br>  |
| Qy<br>Dp  | 2821         | ttttgtattgcagtcgataattggcttcaggtgagtacgacacaactcaattttatatca 2880<br> |
| Oy<br>Bp  | 2881         | tcttcgtgggcgttttgtttgccggtccaagcagcagccagtatttggcttactccacg 2940<br>  |
| Qy<br>Dp  | 2941<br>2941 | agtttaccaaggctcggtcggctgcgaactatatcctctggctgcggacattgaagccg 3000<br>  |
| Qy<br>Dp  | 3001         | accatccgcgaaacggaggagaacaagaaaaaggcccagtgggtgg                        |
| Oy<br>Dp  | 3061         | otogaggacattgaattcaggtatcgtcaacgtgattcggctcgagttctccgcggggtt 3120<br> |
| oy<br>op  | 3121         | tecatgacaategagecaggacaatttgtagettatgtgggegettetggetgtgggaag 3180<br> |

| 1240                                                              | 300                         | 3360                                                              | 3420                                                                                                       | 3480                                                                | 3540<br>3540                                                      | 3600                                                                | 3660                          | 3720<br>3720                                                      | 3780<br>3780                                                       |                      | FEB-2001                                                                       | 0.R.<br>on (US)                                                               |   |
|-------------------------------------------------------------------|-----------------------------|-------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------|----------------------|--------------------------------------------------------------------------------|-------------------------------------------------------------------------------|---|
| aacgttgatcgctttgtcggaacgattctacgacccgacctcgggccgaatttcattt 32<br> | tggtc 3<br>     <br>TGGTC 3 | caacaggaaccacactttaccaaggctccgttcgcgagaatgtgacgttggcctcgaa 3:<br> | <pre>gaattatcagaagagctttgtcaaggacgccttcccgcaaggccaatgctttggatt 3                                    </pre> | ttgtcatctctttaccagaaggctttgaaacgccttgcggctcaacgagggatgcagttc 3/<br> | cggcgggcaacgacagcggatcgccatcgcaagagcattgattcgaaatccaaagctg 3:<br> | ttgctacttgacgaagcgacgtcagccctcgacacgcaatcggaacgtctggttcaagct 3 <br> |                               | attoggaatgttgatgttattttgtgtttgcoaacgggagaatcgccgaaacgggcact 3<br> | cacgeggaactacaacgactgagaggaagatattacgagatgtgtttggcacaatcttta 3<br> | accaagcatga 3792<br> | A linear PAT 22-                                                               | lkerts,0. and Crasta, detoxification ); Curagen Corporati a" ntrons" 5 others |   |
| 검그업                                                               |                             |                                                                   | 0000                                                                                                       | 1 ttç                                                               | 1<br>1<br>1<br>1<br>1<br>1<br>1<br>1                              | 1=t                                                                 | 1<br>- 9<br>- 0<br>- 0<br>- 0 | 1 at                                                              | 1 CAC                                                              | 1 ga<br>1 GA         | S N N S                                                                        | r r r                                                                         |   |
| 3181                                                              | 4 4                         | 3301                                                              | 3361                                                                                                       | 342                                                                 | 348                                                               | 354<br>354                                                          | 360                           | 366                                                               | 372                                                                | 378                  | RESULT 2 AXO76850 LOCUS DEFINITION ACCESSION VERSTON VERYWORDS SOURCE ORGANISM | REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICE .                             | • |
| Q<br>B                                                            | Qy<br>Db                    | QY<br>Db                                                          | QY<br>Db                                                                                                   | Qy<br>Dp                                                            | QY                                                                | oy<br>B                                                             | Q<br>D                        | Q<br>D                                                            | Oy<br>Db                                                           | QY<br>Db             | AXE<br>LCA<br>ACE<br>SCE                                                       | HH . 18                                                                       | 5 |

Query Match 91.1%; Score 3454.8; DB 6; Length 3999; Best Local Similarity 96.1%; Pred. No. 0;

| tctcgacc<br>                                                                                                 | 1160 CAAAACCTGGCATTTGCCTACCCCTCCCGACCATCTCCCAGGTTCCAAC 121                | <pre>1195 ttgacaattccagctggcaagacgacggcctcgtcgtcgttgcatcaggtagcgaaaagc 125 11111111111111111111111111111111111</pre> | 5 acaatggtcggcttacttgaacggtggtatctgcccagttcggggaggatattacttgat 13<br> | S gggttggaacte<br> | Oy 1375 caggaacctgtgtttcgtggcacaatcttccagaacattgccaacggttcatggat 1434<br>                                                   | Oy 1435 gagcaacgagatctgcctcgcgaaaacaaatggagcttgtgcaaaaagcttgcaaaagcc 1494 | 95 agcaatggcgacgtgttcatte<br>                                         | Oy 1555 cgagccggagccttgagtggaggtcaacgacaacganttgcaatcgcacgaagtatcata 1614 | Oy 1615 toggatcccaagatcctgttactcgatgaagctaccagcgccttgacccgaaggcggag 1674 | Oy 1675 aaagtggtccaggaggcettgaaccgagtgtccaaagaccgcactactttggtcattgcc 1734 | Oy 1735 cacaaactagccactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaaaatc 1794 | Oy 1795 gtcgagcaaggcacacacacagaattgatcgaattcggctgtcattacgccgcac 1849 | 0 tggtgcgtgcacaggacctcg<br>                                             | ψ – <b>4</b> ,                                                           | O ccacatctcaagctggagacctggagaagcggaaggtgccggtcgggac<br> | 2030 cgctcctaaaatgcatcctaatcatgttctacgaacaaaaaatctctactggtgcttct 208 [   | Oy 2090 tgttgtcaacaataacggttctgatatgcgcggccacatttccaggacaagccttttgt 2149  |
|--------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|--------------------|-----------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------|-----------------------------------------------------------------------|---------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------|
|                                                                                                              |                                                                           |                                                                                                                      | о п                                                                   |                    | 0 1                                                                                                                         | 0 1                                                                       | <b>G</b> L                                                            | 0 0                                                                       | 0 0                                                                      | 0 0                                                                       | 0 0                                                                       | о п                                                                  | 0 0                                                                     | φΔ                                                                       | 0 Д                                                     | 0 0                                                                      | O Q                                                                       |
| Matches 3658; Conservative 4; Mismatches 126; Indels 2 1 atgcagatgaatcggagaaacctcgaccaaaccaagatggcagtgagtcct | Qy 61 cctccccagaaaaggaaaccgaaggcagtatttcagactatctacgaatcttcagatat 120<br> | Oy 121 gccgacaaatacgactggactctcaatgtcatcgcgctcatctgcgccatcggatccggg 180                                              | Qy 181 gcttccttcctctgatgtcgatcatcttcggtagcttcaccaacaagttcaacaatac 240 | <b>€</b> €         | <pre>Qy 301 ttogtctacctctttattgggaagtttgtcctcacgtacgtttccacggctgccattacc 360<br/>                                    </pre> | tgcaccttgcgg 42<br>              <br> GCACCTTGCGG 43                      | Oy 421 caagagtctggcatttcgacaagcagtgagcaatggagcactcargtcactacc 480<br> | caggcactt 5<br>             <br>CAGGCACTT 5                               | Qy 541 tcaatgttctttctgcatttgtggtcgctttggcgtctcagtggaagctagct             | ooggeatctgcatagcaattgatgcc 66                                             | cctcgcagaaga<br>            <br> CTCGCAGAAGA                              | cgaaaaatat 7:<br>                                                    | Oy 781 gatgtcttttgcagcaagcaacaccaagaaggaaggaagtcgcaaataatggsgtc 840<br> | Oy 841 ttgttctcaactgagtacttttgcatttacgctgtgtatcgcactggcctttggaaa 897<br> | ctttactgttgtc<br>                                       | Oy 958 ctttccgtcaccttagcagccacgtccatctcaatgcttgcgccttcaggttcagtcgtt 1017 | Oy 1018 taccaacgccgcatcttcgg-ctccgaattattcagtatcattgacaaacccacgcagct 1076 |

| Qy       | 1077 | ccttctggaaagcagccagaggctgctaggtcaaattgagatc<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 134 |
|----------|------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ò        | 1135 | ggcatttgctaccctccgaccatctgcccagtacttcgagatttcaa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 194 |
| ò        | 9 6  | rancettocontracetroccorrectorrentations and transfer treatments to the contract of the contrac | 54  |
| qq       | 7    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 643 |
| ý d      |      | aatggtcggcttacttgaacggtggtatctgcccagttcggggaggatattacttgat<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 114 |
| ò        | ) ∺  | dqttqqaactqqqacaatacaatqtqaaatqqctqaqaaqcqcattcqcctcqt                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 7.  |
| G 60     |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 66  |
| οy       | 7    | ggaacctgtgttgtttcgtggcacaatcttccagaacattgccaacggtttcatggat<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 34  |
| <b>Q</b> | 1400 | AGGAACCTGTGTTTTCGTGGCACAATCTTCCAGAACATTGCCAACGGTTTCATGGAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 59  |
| ογ       | 1435 | 38gatctgcctcgcgaaaaacaaatggagcttgtgcaaaaagcttgcaaagcc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 94  |
| qq       | 1460 | Ö                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 118 |
| ογ       |      | 6-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 54  |
| qq       | 1519 | - g                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 18  |
| οy       |      | cata                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 14  |
| qq       |      | ⋖                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 37  |
| οy       | 1615 | <u>6</u> -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 74  |
| QQ       |      | - ပွ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 26  |
| οy       | 1675 | <u> 0</u> -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 34  |
| g        | 1698 | - <u>U</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 57  |
| 0y       | 1735 | o                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 94  |
| qq       | 1758 | E-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 17  |
| οy       | 1795 | ų-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 49  |
| q        | 1818 | ي -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 77  |
| οy       | 1850 | <u>ت</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 60  |
| qa       | 1878 | - <u>0</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 37  |
| ογ       | 1910 | ρ.<br>1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 69  |
| qq       | 1938 | G-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 97  |
| ογ       | 1970 | t -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 29  |
| đ        | Ų,   | - [→                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 57  |
| οy       | 2030 | t 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 68  |
| qq       | 2058 | CICCTAAAATGCATCCTAATCATGTTCTACGAACAAAAAATCTCTACTGGTGCTTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 17  |

| <u>~</u>                                                          | <i>ර</i> බ                                                        | 67 B                                                               | ଟ ଅ                                                                | රි බි<br>                                                          | 6 B<br>                                                        | රි කි (                                                    | න කි <sub>ව</sub>                                                  | ි කි ·                                                              | ි <b>සි</b>                                                               | 243                                                            |                                                                 | ⊒.ŏ                                                             |                                                                |                                                                    | <b></b>                                                          | <u></u>                                                            |                                                                  |
|-------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------|------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------|-----------------------------------------------------------------|-----------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------------|------------------------------------------------------------------|
|                                                                   |                                                                   |                                                                    |                                                                    |                                                                    |                                                                |                                                            |                                                                    |                                                                     |                                                                           |                                                                |                                                                 |                                                                 |                                                                |                                                                    |                                                                  |                                                                    |                                                                  |
| 2209                                                              | 2269                                                              | 2329                                                               | 2389                                                               | 2448                                                               | 2508                                                           | 2568<br>2597                                               | 2628<br>2657                                                       | 2688                                                                | 2748                                                                      | 2808<br>2835                                                   | 2864                                                            | 2924                                                            | 298 <b>4</b><br>3015                                           | 3044                                                               | 3104                                                             | 3164                                                               | 3224<br>3255<br>3284                                             |
| 0 tttgagattgctcactgtcttcgagttgagtggtcatggggcacaggaacgggcagact<br> | 0 tttatattctgatgttctttgtcgtggctctaggaaatctagtaggatattcacgattg<br> | 0 gctggacatgcaacgttatttcacaagttgtcacccatcgctatcaagccgcaatgttcc<br> | O aacgagtactggatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctc<br> | 0 tcacatcgcaactgtcagctctacccacgcagttgcaagagttgatatcagcaaatt-tt<br> | 9 ctcatttatatcgttgtcggtcaacatcgtctcgagcagtgctctaccactagcctatgg | 9 atggaaactgggcctggtggttgtgtgtggtgcacttccaccctgctttggctggc | 9 cctcagaattcgtctagagacgaagctagaagccggaaactcggcaaactttgcagaaag<br> | 9 tgctgggcttgcaagcgaragcagttaccgcgatccggaccgtctcatctttgactctcga<br> | 9 aggocatgitcitccaacagiacicggacaigitigagcaaggicitgciaagaicaiccaa<br>    : | 9 agcttttggtttggacgatgtttggtttcacttgtcacagtcgatgagttttggct<br> | 9 attgccctgggattttgtattgcagtcgataattggcttcaggtga-gtacgacaca<br> | 5 acteaatttatateateatettegtgggegttttgtttgeeggteeaageageageeggte | 5 tttggettactccacgagttttaccaaggetcggtcggctgcgaactatatcctctggct | 5 gcggacattgaagccgaccatccgcgaaacggaggagaacaagaaaaaaggcccagtggg<br> | 5 tggatgcctgtcgacctcgaggacattgaattcagtatcgtcaacgtgattcggctcg<br> | 5 agttctccgcgggggtttccatgacaatcgagccaggacaattgtagcttatgtgggcgc<br> | ttctggctgtggcaagtcaacgttgatcgctttgtcggaacgattctacgacccgacctc<br> |
| 215(                                                              | 221(                                                              | 227(                                                               | 233(                                                               | 239(                                                               | 2449                                                           | 2509                                                       | 2569                                                               | 2629                                                                | 2689                                                                      | 2749                                                           | 2806                                                            | 2865                                                            | 2925                                                           | 3016                                                               | 304:                                                             | 3105                                                               | 3165<br>3196<br>3225                                             |
| Qy<br>Db                                                          | Oy<br>Dp                                                          | Oy<br>Dp                                                           | 95<br>Pp 03                                                        | oy<br>Db                                                           | oy<br>D                                                        | Qy<br>Db                                                   | QY                                                                 | Qy<br>Dp                                                            | Qy<br>Db                                                                  | oy<br>Ob                                                       | Oy<br>Ob                                                        | QY<br>Db                                                        | Qy<br>Db                                                       | oy<br>Db                                                           | QY<br>Db                                                         | oy<br>Db                                                           | 99 O                                                             |

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Appendillus nidulans ATP-binding cassette multidrug transport protein ATRC (atrC) gene, complete cds.
AF071410
AF071410.1 GI:5456698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waard, M.A.

The role of ABC transporters from Aspergillus nidulans in protection against cytotoxic agents and in antibiotic production Mol. Genet. 263 (6), 966-977 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emericella nidulans.
Emericella nidulans
Eukarycta; Fungl; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurociales; Trichocomaceae; Emericella.
1 (bases 1 to 6120)
Andrade, A.C., Van Nistelrooy, J.G., Peery, R.B., Skatrud, P.L. and
3256 GGGCCGAATTTCATTTGCACACGAGAATATTGCAGAAATGTCGCCGCGCTTGTACCGCGG 3315
                                   3404
                                                                                                          3435
                                                                                                                                3736 CGCCGAAACGGGCACTCACGCGGAACTACAACGACTGGAGGAGGAGATATTACGAGATGTG 3795
                                                                                                                                                                                             Submitted (09-JUN-1998) Phytopathology, Wageningen Agricultural University, P.O.Box 8025, Wageningen 6700 EE, The Netherlands Location/Qualifiers
                                                                                                                                                                                3465 acgagggatgcagttctccggcgggcaacgacagcggatcgccatcgcaagagcattgat 3524
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/strain="W6-096"

/db_xref="taxon:162425"

/chromosome="V11"

join(<628. .747,813. .1000,1047. .1703,1761. .3948,

/gene="atrc"
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                                                                                    gacgttggccctcgaagccgaattatcagaagactttgtcaaggacgccttcccgcaag
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DEATSALDTESEKIYQKALEGAARDGDRLTVAVAHRLSTIKDANVICVFFGGKIAEMG
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                                                                                           /function="putatively involved in multidrug
/note="similar to MDR; ABC transporter C"
                                                  Join(628. .747,813. .1000,1047. .1703,1761.
/gene="atrc"
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GTCAGGAAGTTTGATGAATATCTGGTGGAGGCGCATAAGGTCGGTAAGAAGATCTCGCCG 1581
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                                                                                                                                                                                                   ttttggaaaggttttcgcatgtatcagaatggcgaggttgccgacgttggcaaagtcttt
                                                     aataatggsgtcttgttctcaactgagtacttttgcatttacgctgctatcgcactggcc
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| 900                                                            | 847                                                                    | 1907                                                              | 96        | 0 00                                | 081<br>900                                                    | 141<br>960                                                             | 201<br>020                                                     | 261<br>080                                                         | 321<br>140                                                     | 381<br>200                                                     | 441<br>260                                                    | 499                                                           | 559<br>380                                                                | 619<br>440                                                         | 679                                                            | 739<br>559                                                   | 799<br>618                                                          | 858                                                               |
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| qq                                                             | Oy<br>Dp                                                               | o d                                                               | Oy<br>Dp  | Qy                                  | Qy                                                            | Oy<br>Dp                                                               | Oy<br>Dp                                                       | Qy<br>Dp                                                           | Qy<br>Db                                                       | Qy<br>Dp                                                       | oy<br>Ob                                                      | 70 dg                                                         | Oy<br>Db                                                                  | Oy<br>Dp                                                           | Oy<br>Dp                                                       | Qy<br>Db                                                     | Oy<br>Db                                                            | δy 4                                                              |

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Skatrud, P. Luther, de Waard, M.A., Andrade, A.C. and
Multiple drug resistance gene atrD of Aspergillus
Patent: US 6228615-A 1 08-MAY-2001;
Location/Qualifiers
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Skatrud, P. Luther., de Waard, M.A., Andrade, A.C. and Peery, R. Brown.
Multiple drug resistance gene atrD of Aspergillus nidulans
Patent: Location/Qualifiers
1. 4002
                                                                                                                                                                                          tgtgtttgccaacgggagaatcgccgaaacgggcactcacgcggaactacaacgactgag 3743
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                                                                                                                                                                  TIGATTAAGGCTIGCAAGGACGCTAATATCTACGACTTCATCATGTCGTCCCCCGGAGGG
                                                         cgattctacgaccccgacctcgggccgaatttcatttgcacacgagaatattgcagaaatg
                                                                                                                           ggetecgttegegaatgtgaegttggeectegaageegaattateagaag-agetttg
                                                                                                                                           GGCACCATCAAGGAAAACATCTTACTTGGTATTGTCGAAGATGACGTACCGGAAGAATTC
                         tttgtagcttatgtgggcgcttctggctgtggcaagtcaacgttgatcgctttgtcggaa
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AR149777
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48.6%;
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Best Local Similarity 48.6
Matches 1731; Conservative
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TITLE
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|---------------|---------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------------|---------------------------------------------------|----------------------------------------------------------|------------------------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------|-----------------------------------------------------------------|-------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------|
|               | 2 aagcagagcaatggagcactcargtcactaccaatggcaaccgtatacaaaca | gtggtcgctttggcgtctcagtggaagctagctttaatcaccatgtccgtcatcctgc<br> | <pre>2 attttcctggtcaccggcatctgcatagcaattgatgccgctcaggaggccaggatcacc</pre> | aggatctactcacgcgcgctgtcctcgcagaagagtcttatcatccatc | catgettetacgeccagaagaaatggtegaagaatatgatgtetttgeageaagea | caccaagaaggaagaagaatcgccaaataatggsgtcitgttctcaactgagtacttt | tgcatttacgctgctatcgcactggccttttggaaaggttttcgcatgtatcagaatggc<br> | gaggttgccgacgttggcaaagtctttactgttgtcctttccgtcaccttagcagcacg | tocatcicaatgottgogocttcaggitcagitgitaccaacgccgcatcttgggctcc<br> | gaattattcagtatcattgacaaacccacgcagctcgaccctctcgaccttctggaaag | cagccagagggctgcctaggtcaaattgagatccaaaacctggcatttgcctaccctcc | cgaccatctgcccaagtacttcgagatttcaacttgacaattccagctggcaagacgacg | gccttgtcgttgatcaggtagcgaaagcacaatggtcggcttacttgaacggtggii | tatctgcccagttcggggaggatattacttgatgggttggaactgggacaatacaatgtg<br> | aaatggctgagaagccgcattcgcctcgttcaacaggaacctgtgttgtttcgtggcaca |
|               | 504<br>604<br>502<br>664                                | 9 0                                                            | 622<br>784                                                                | 682                                               | 742                                                      | 802<br>964                                                 | 862                                                              | 922                                                         | 982                                                             | 1042                                                        | 1102                                                        | 1162                                                         | 1222                                                      | 1282                                                             | 1342                                                         |
|               | 6 6 6                                                   | Oy<br>Dp                                                       | oy<br>B                                                                   | g 63                                              | 6y<br>Gp                                                 | 0y<br>Dp                                                   | Qy<br>Dp                                                         | Oy<br>Dp                                                    | δ α                                                             | \$ B                                                        | 9<br>9                                                      | Oy<br>Dp                                                     | Oy<br>Dp                                                  | Oy<br>Dp                                                         | ολ                                                           |

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                       gagttgatatcagcaaattttctcat--ttatatcgttgtcggtcaacatcgtctcgagc
                                       GETGITAGCGGTGTGTCTAGGCACCATCTTGATGACCTCCACGACCCTAGGAGCGGCT
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Srub2933 4050 bp mRNA linear PLN 10-DEC-1997
Aspergillus fumigatus multidrug resistance protein 1 (mdr1) mRNA,
complete cds.
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1 (bases 1 to 4050)

Tobin, M.B., Peery, R.B. and Skatrud, P.L.
Genes encoding multiple drug resistance-like proteins in
Aspergillus funigatus and Aspergillus flavus
Gene 200 (1-2), 11-23 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-JUL-1996) Lilly Research Laboratories, Eli Lilly and
Company, Lilly Corporate Center, Indianapolis, IN 46285-0424, USA
Location/Qualifiers
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                                                                                                cogaacgacaatagcagtggcgcaccgactttccactattcggaatgttgatgttatttt 3683
                                                                                                                                                   Aspergillus fumigatus.
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                cgccatcgcaagagcattgattcgaaatccaaagctgttgctacttgacgaagcgacgtc
             agocotogacacgoaatoggaacgtotggttcaagotgcootogatgaggoatocacgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="anamorph=Aspergillus fumigatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fumigatus
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/strain="10AF/86/10"
/db_xref="taxon:5085"
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| GGCCGGTACTACGAGCTG 3972
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KEYWORDS
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MEDLINE
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TITLE
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PKVLLLDBAFSALDSESEKVVQAALDAAARGRTTIAVAHRLSTIQNADIITVFFDQGKI
VESGTHHELIRNKGRYFELVNLQSLGKTH"

17 a 995 c 1031 g 1057 t 11; 1021 235 295 355 361 421 481 541 415 601 475 535 595 895 661 721 781 655 841 715 901 775 961 835 Gaps gatatgccgacaaatacgactggactctcaatgtcatcgcgctcatctgcgccatcggat ccggggcttcccttcctctgatgtcgatcatcttcggtagcttcaccaacaagttcaaca attacaattogggcgacgggaqtcctgaagcgttcaaggccgatgtggatcatttcgtcc CTGGTGCCGCTCTTCCCTTGTTCACATTCTTCGGTTCACTAGCCTCAGCGTTCCAGG GCATATCTCTGGGTACTATGCCTATCATGAGTTCTATCACAAACTGACTAAGAATGTGC ttaccatttcagctatacgaaccactcgaactcttcgacgagtgttccttgaatgcacct TCATTTATACTGGCGAACATCTCACACAGAAGATCCGTGAAAATTATCTTGAGGCTATCC CATTCGCCACATTTGTAACCGCATTTATTGTCGCCTACGTCAAGTATGGAAGTTGGCTC taatcaccatgtccgtcatcctgccattttcctggtcaccggcatctgcatagcaattg atgccgctcaggaggccaggatcaccaggatctactcacgcgccgctgtcctcgcagaag aagtettateateeateeggaeagteeatgetttetaegeeeagaagaaaatggtegaaa TTGTGAAGTACAGCAAGAAATCTATTGAAAGTTATGGTGCTGGTGGAACTGTCGCGGAAG AAGTCATCAGCTCCATTCGGAATGCTACCGCTTTCGGCACTCAGGATAAGCTCGCCAAGC aatatgatgtettttgeageaageaceaceagaagggaagaagaaategeeaaataatg AATACGAAACCCATCTGGCTGAGGCTGAAAATGGGGCGTCAAACAACAAGGTCATCCTTG gsgtcttgttctcaactgagtacttttgcatttacgctgctatcgcactggccttttgga 87; Length 4050; Indels Score 450.6; DB 8; Pred. No. 3.7e-115; 0; Mismatches 1869; Query Match
Best Local Similarity 47.5%;
Matches 1769; Conservative ø 967 BASE COUNT 116 302 176 362 236 356 542 416 502 422 296 482 842 476 662 536 722 969 782 929 902 716 176 862 836 ORIGIN

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1435 TGGGATCTCGCTTCGTTGTCGGTAAAGAAGT---CAACGTGGGCCAAGTTCTGACAGTTT 1138 1492 1918 1792 tttaccaacgccgcatcttcggctccgaattattcagtatcattgacaaacccacgcagc tectiticegicacettageagecaegiceateteaatgetigegeeticaggiteagieg TGATGTCTATCCTGATCGGTTCGTTCAGTTTGGGCAACGTCGCCCCAATGGTCAGGCCT tgacaattccagctggcaagacggccgtcgtcgtgcatcaggtagcggcaaaagca CTGTTGTCGGCTTGGTGGAGCGCTTTTACCTTCCAGTAGGAGGCCAGGTATTGCTGGACG cccacaaactagccactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaaaa tegacectetegacecttetggaaageagecagagggetgeetaggteaaattgagatee TGGACCCCTATTCTGACGAAGGAACGTACTCGACCATTTTGAAGGAAATATCGAATTTC aaaacctggcatttgcctacccctcccgaccatctgcccaagtacttcgagatttcaact TATCGATGCCCGCCGGAAAGACTACCGCATTGGTGGGCCCCATCTGGCTCTGGAAAGAGTA ggttggaactgggacaatacaatgtgaaatgggctgagaagccgcattcgcctcgttcaac GCCATGATATCCAAACCTCAACCTCCGTTGGCTGCGACAGCAGATCTCTTGTCAGCC agcaacgag---atctgcctcgcgaaaaacaaatggagcttgtgcaaaaagcttgcaaag ccagcaatggcgacgtgttcattaatgagcttccgaacggttatgagactgaagttggcg 1679 TGGCCAATGCTCATGATTTTATTATGGCTCTGCCTGAAGGTTACGATACGAATGTGGGTC agcgagccggagccttgagtggagtcaacgacaacgaattgcaatcgcacgaagtatca agaaagtggtccaggaggccttgaaccgagtgtccaaagaccgcactactttggtcattg aggaacctgtgttttcgtggcacaatcttccagaacattgccaacggtttcatggatg AGGAACCTGTTCTTTCAGCACCACGATCTTTAGAAACATCGAACATGGCTTGATTGGCA tatoggateceaagatectgttaetegatgaagetaeeagegeeettgaeeegaaggegg CTCACCGTTTGTCAACAATCAAAACAGCCCACAACATGTTGCCATGGTCGGCGGAAAGA tgcgtgcacaggacctcggggctgacgaacaacaagaacatgagaagacctgcacgaaa TGGACGCCGATGATTTTGGTCAAGAGGGGTTACTCGCATCAAGACTGCAGTTAGCAGCT ...----tggagacctggagaagcggaaggt aggoagoacgagaagotgotggtgaacg----accggcacttgagcgcactcacaccac tgccacatctcaagc-----1016 1139 1199 1076 1136 1319 1379 1316 1376 1259 1196 1256 1439 1499 1559 1436 1619 1553 1739 1613 1859 926 1493 1799 1919 1673 1733 1793 1979 1853 2039 1913 ò q ò 셤 à QQ ò ద ö g ò qq ò g δ d ò g ò . g ö a g g ò Š q g å ò à d ç g ð g

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GTATGATGATTGGTGTATCGTATCATGTTCTCGAACTATGGTCTCGGTTTCTGGA aaggttttegeatgtatcagaatggegaggttgeegaegttggeaaagtetttaetgttg

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| å                | 2007       | 100                                                                        |  |
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| 5                |            |                                                                            |  |
| g                | 2219       | AAAAATCGGTTTCGAGTGCCGTTCTATCTAAGAAAGTCCCCGAGCAGTTCGAGAAGTATT 2278          |  |
| δò               | 2041       | 60                                                                         |  |
| g ,              | 2279       | 233                                                                        |  |
| ያ የ              | 2096       | caacaataacggttctgatatgcgcgccacatttccaggcaagcctttttttt                      |  |
| 3 8              | <b>.</b> u | 500                                                                        |  |
| 2 2              | 2399       | ACCCAAGGCAATTAGCACGTCTCGTTACCCGAATCAATGTTTCACAAACTCAGGCATG 2458            |  |
| δλ               | 2201       | gggcagacttttatattctgatgttctttgtcgtggctctaggaaatctagtaggatatt 2260          |  |
| QQ               | 2459       | ACGCGAATTTCTGGTCCTTGATGTTCTTCGTGGTTGGAATTGCTCAATTATCAGCCTGT 2518           |  |
| δ                | 26         | 232                                                                        |  |
| g                | 2519       | CTATCAATGGTACAGCATTTGCTATTTGTTCGGAGAGACTCATTCGCCGAGCTAGAAGTC 25/8          |  |
| δ<br>D<br>D<br>D | 2321       | caatgitccaacgagtactggatcaagacatcgaactcctcgacatcccggagcaaatti 2380<br>      |  |
| δλ               | 80         | ctggtgctctcacatcgcaactgtcagctctacccacgcagttgcaagagttgatatcag 2440<br>      |  |
| qq               | 2639       | CCGGTGCCTTGACGTCCTTCTTATCAACAGAGAAGAATCTGTCGGGGGGTTAGCGGAG 2698            |  |
| Oy<br>Dp         | 2441       | <pre>caaattttctcatttatatcgttgtcggtcaacatcgtctcgagcagtgctctaccac 2498</pre> |  |
| ó                | თ          | 255                                                                        |  |
| - Q              | 75         | 281                                                                        |  |
| δŏ               | 2559       | tggctggctacctcagaattcgtctagagacgaagctagaagccggaaactcggcaaact 2618          |  |
| QQ               | 2816       | CATGCGGCTTCCTCAGATTCTACATGCTTGCTCAGTTCCAGCAACGATCGAAGTCTGCCT 2875          |  |
| Oy<br>Db         | 2619       | ttgcagaaagtgctgggcttgcaagcgaagcagttaccgcgatccggaccgtctcatctt 2678<br>  1   |  |
| l è              | 2679       | 273                                                                        |  |
| 2 G              | 93         | TCACTCGCGAACAAGATGTCTGGGGCGTTTACCACGACCAGCTACAAAAACAGGGACG 299             |  |
| oy<br>Dp         | 2739       | gatcatccaaagcttttggttttggtttttggttttcacttgtcacagtcgatgga       2798        |  |
| δλ               | 2799       | 285                                                                        |  |
| qq               | 3054       |                                                                            |  |
| οy               | 2859       | gacacaactcaattttatatctctcgtgggcgttttgtttg                                  |  |
| qq               | 3114       | CAGCATCTTCCGCTTCTTCGTCTTTTTGATTCTTTTTGGTGCGCATCAGCCGG 3173                 |  |
| ور<br>م          | 2919       | ccagtatttggcttactccacgagttttaccaaggctcggtcgg                               |  |
| 3                |            | 1 6                                                                        |  |
| g d              | 3234       | ctggctgcggacattgaagccgaccatccgcgaaacggaggagaacaagaaaaaggccc 3038<br>       |  |
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4569 bp DNA linear PLN 03-FEB-2000 Emericella nidulans ABC-transporter (abcD) gene, complete cds. AF173826 AF173826.1 GI:6856158
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Nascimento, A.W., Terenzi, M.F., Goldman, M.H.S. and Goldman, G.H.
Direct Submission
Submitted (29-JUL-1999) Ciencias Farmaceuticas, FCFRP-Universidade
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                ccgcggccatatgtctttggtccaacaggaacccacatttaccaaggctccgttcgcga 3338
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Emericella nidulans

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichhocomaceae; Emericella.

1 (bases 1 to 4569)

Nascimento, A. M., Terenzi, M.F., Goldman, M.H.S. and Goldman, G.H

Molecular characterization of ABC-transporter encoding genes appergillus shed
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                                                                  gacetegggeegaattteatttgeacaegagaatattgeagaaatgtegeegegttgta
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APSSTTATPADKEHRPKSSSSNNAVSVNEVDALIAHLPEDERQVLKTQLEEIKVNISF
FGLWRYATKMDILIMVISTICAIAAGAALPLFTILFGSLASTFQRIMLYQISYDEFYD
ulo, Av. do Cafe S/N, Ribeirao Preto, SP 14040-903, Brazil
Location/Qualifiers
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WSEEGEKLETVEGEIEFRNVHFRYPTRPEQPVLRGLDLTVKPGQYVALVGPSGCGKST
TIALLERFYDAIAGSILVDGKDISKLNINSYRSFLSLVSQEPTLYQGTIKENILLGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDDVPEEFLIKACKDANIYDFIMSLPEGFNTVVGSKGGMLSGGGKORVAIARALLRDP
KILLLDEATSALDSESEKVVQAALDAAARGRTTIAVAHRLSTIGKADVIYVFDQGKIV
ESGTHSELVQKKGRYYELVNLQSLGKGH"
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Pred. No. 1.2e-107;
0; Mismatches 1820;
                                                                                               /organism="Emericella nidulans"
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/gene="abcD"
/product="ABC-transporter"
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/db_xref="G1:6856159"
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| 1926 | 1731<br>1986                                                | 1791<br>2046                                                     | 1851<br>2106                                                | 1875                         | 1935<br>2226                                 | 1995<br>2286                                              | 2040                                              | 2100                                                        | 2160                                                            | 2220                                                             | 2280                                                           | 2340                                                         | 2400                                                             | 2458                                                          | 2518<br>2826                                           | 2578                                           | 2638                                                            | 2698                                                             |
|      | gagaaagtggtccaggaggcttgaaccgagtgtccaaagaccgcactactttggtcatt | geccacaaactagccactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaaa<br> | atcytcyaycaagycacacacacyaattyatcyaattcyyctytcattacyccycacty | gtgcgtgcacaggacctcggggct<br> | gacgaacaacaagaacatgagaagacctgcacgaaaaggcaggc | gaacgaccggcattgagcgcactcacactcgccacatctcaagctggagacctggag | aagoggaaggtgccggtcgggactttgggctactcgctcctaaaa<br> | tgcatcctaatcatgttctacgaacaaaaaatctctactggtgcttcttgttgtcaaca | ataacggttctgatatgcgcggccacatttccaggacaagccctttgttttcgagattg<br> | ctcactgtcttcgagttgagtggtcatgcggcacaggaacgggcagacttttatattctg<br> | atgiteitigiegigetetaggaaatetagiaggatatteaegatiggetggaeatge<br> | aacgttatttcacaagttgtcacccatcgctatcaagccgcaatgttccaacgagtactg | Gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa<br> | ctgtcagctctacccacgcagttgcaagagttgatatcagcaaatttctcatttata<br> | togttgtoggtcaacatcgtctcgagcagtgctctaccactagcctatggatgg | ggcctggtgtttgtttggtgcacttccacccctgcttttggctggc | cgtctagagagaagatagaagccggaaactcggcaaactttgcagaaagtgctgggctt<br> | gcaagcgaagcagttaccgcgatccggaccgtctcatctttgactctcgaaggccatgtt<br> |
| 1867 | 1672<br>1927                                                | 1732<br>1987                                                     | 1792<br>2047                                                | 1852                         | 1876<br>2167                                 | 1936<br>2227                                              | 1996                                              | 2041                                                        | 2101                                                            | 2161                                                             | 2221                                                           | 2281                                                         | 2341                                                             | 2401                                                          | 2459                                                   | 2519<br>2827                                   | 2579                                                            | 2639                                                             |
| qq   | QQ<br>QQ                                                    | Qy<br>Dp                                                         | 0 <u>y</u>                                                  | ç<br>G                       | S S                                          | QY<br>Dp                                                  | oy<br>Ob                                          | Oy<br>Op                                                    | Qy<br>Db                                                        | Qy<br>Dp                                                         | Qy<br>Dp                                                       | Oy<br>Db                                                     | Oy<br>Dp                                                         | Qy<br>Dp                                                      | S S                                                    | Oy<br>Dp                                       | oy<br>B                                                         | QY                                                               |

3177 2817 3121 3241 2997 3300 3480 3237 3540 3297 3600 3061 3181 2937 GTCGAAGATGACGTACCGGAAGAATTCTTGATTAAGGCTTGCAAGGACGCTAATATCTAC 3720 || || || 1111 || || 19 3721 GACTICAICATGICGCTCCCGTAAGITCAIATITCTGICCTICAICCIAIACTGGICCG 3780 gocottogatgaggoatcoacgagcogaacgacaatagcagtggogcaccgactttcoact 3660 cogaccateegegaaacggaggagaacaagaaaaaaggeeeagtgggtggatgeeetgte 3057 -----agaaggetttgaaacgeettgcggeteaacgagggatgcagttc 3480 CTAACATGCAACAATAGGGAGGGCTTTAATACAGTTGTTGGCAGCAAGGGAGGCATGTTG 3840 ttgctacttgacgaagcgacgtcagccctcgacacgcaatcggaacgtctggttcaagct 3600 2944 GCTTGCGAGGCTACATCGTCTATCCGCACAGTTGCGTCATTAACCCGGGAAAGGGATGTC 3003 TGGGAGATTTACCATGCCCAGCT--TGACGCACAAGGCAGGACCAGTCTAATCTCTCTCT ggattttgtattgcagtcgataattggcttcaggtgagtacgacacaactcaattttata tcatcttcgtgggggttttgtttgccggtccaagcagcagcagtatttggcttactcc CCACAAATTGATAACTGGTCTGAAGGGGGGGGAGAAGCTCGAAACGGTGGAAGGTGAAATC 3238 tttgcacacgagaatattgcagaaatgtcgccgcgcttgtaccgcggccatatgtctttg ctccaacagtactcggacatgttgagcaaggtcttgctaagatcatccaaagcttttggt ttggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgccct-g TGAGGTCATCCCTGTTATATGCGTCGTCGCAGGCACTTGTTTTCTTCTTGCGTTGCGCTCG 3182 TITGITTCTCCGAGATTCTCTTTGGTGCTCAATCCGCGGGCACCGTCTTTTCCTTTGCAC aagtcaacgttgatcgctttgtcggaacgattctacgacccgacctcgggccgaatttca acgagittiaccaaggotcggtcggctgcgaactatatcctctggctgcggacattgaag gaagccgaattatcagaag-agctttgtcaaggacgccttcccgcaaggccaatgctttg gattttgtcatctctttacc-----3661 2699 3004 2759 3062 2818 3122 2878 2938 2998 3301 3178 3358 3417 3437 3781 3481 3841 3541 3601 3961 90 04 05 οy oy Oy oy Oy a οy g οy g

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Submitted (09-JUN-1998) Phytopathology, Wageningen Agricultural
University, P.O.Box 8025, Wageningen 6700 EE, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                           Emericella nidulans.
Emericella nidulans
Eukarjota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eukaryota; Fungi; Ascomycoeae; Emericella.

1 (bases 1 to 6133)
Andrade, A.C., Van Nistelrooy, J.G., Peery, R.B., Skatrud, P.L. a
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Andrade, A.
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                                 Gaps
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                                                                                                                  aattacaattogggcgacgggagtcctgaagcgttcaaggccgatgtggatcatttcgtc
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                                Indels 123;
 Score 424; DB 8; I
Pred. No. 1.2e-107;
O; Mismatches 1820;
Ouery Match
Best Local Similarity 47.5%;
Matches 1759; Conservative
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| 09 1195 ttgacaattc 09 1255 acaatggtcg 09 1255 acaatggtcg 09 1255 acaatggtcg 09 1255 acaatggtcg 09 1315 gggttggaac 09 1315 gggttggaac 09 1315 caggaacctg 09 1375 caggaacctg 09 1375 caggaacctg 09 1375 caggaacctg 09 1375 atgacgaac 09 1552 gagaaagtgg 09 1792 atcgtcgaac 00 1792 atcgtcac 00 1792                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ttgacaattccagctggcaagacgacgtcctcgtcggtgcatcaggtagcggcaaaagc 1254<br> | acaatggtcggcttacttgaacggtggtatctgcccagttcggggaggatattacttgat 1314<br> | tgggacaatacaatgtgaaatggctgaagccgcattcgcctcgttcaa 1374<br> | caggaacctgttgtttcgtggcacaatcttccagaacattgccaacggtttcatgg 1432<br> | -atgagcaacgagatctgcctcgcgaaaaacaaatggagcttgtgcaaaaagcttgcaaa 1491<br> | gccagcaatggcgacgtgttcattaatgagcttccgaacggttatgagactgaagttggc 1551<br> | gagcgagccggagccttgagtggaggtcaacgacaacgaattgcaatcgcacgaagtatc 1611<br> | atatoggatocoaagatoctgttaotogatgaagotaocagogocottgaocogaaggog 1671<br> | gagaaagtggtccaggaggccttgaaccgagtgtccaaagaccgcactactttggtcatt 1731<br> | geccacaaactagecactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaaa 1791<br> | atcgtcgagcaaggcacaccacgaattgatcgaattcggctgtcattacgccgcactg 1851<br> | gegtgcac       | gacgaacaacaagaacatgagaagacctgcacgaaaaggcagcacgagaagctgctggt 1935<br> | gaacgaccggcacttgagcgcactcacactgccacatctcaagctggagacctggag 1995<br> | aagcggaaggtgccggtcgggactttgggctactcgctcctaaaa 2040<br> | catcctaatcatgttctacgaacaaaaatctctactggtgtgttcttgttgtcaaca 2100<br> | aacggttctgatatgcgcggccacatttccaggacaagccctttgttttcgagattg 2160<br> | ctcactgtcttcgagttgagtggtcatgcggcacaggaacgggcagacttttatattctg 2220<br> |
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| 11955<br>2778<br>2838<br>2838<br>2898<br>2898<br>2958<br>2958<br>2958<br>1433<br>3018<br>1433<br>3018<br>1433<br>3018<br>1739<br>1739<br>1739<br>1855<br>1855<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959<br>1959 | ttgacaattccagctggc<br>                                               | acaatggtcggcttactt<br>                                                | ggttggaact<br>         <br>GCCATGACAT                     | caggaacctgtgttgttt<br>                                            | -atgagcaacgagatctg<br>                                                | gccagcaatggcgacgtg<br>     <br>ATGGCGAATCCTCATGAC                     | gagcgagccggagccttg<br>                                                | atatoggatocoaagato<br>                     <br>GTTAGTGACCCAAAATO      | gagaaagtggtccaggag<br>                <br>GAAGGCGTGGTTCAAGC           | gccacaaactagccact<br>                                                 | atcgtcgagcaaggcaca<br>                                              | gtgcgtgcac<br> | gacgaacaacaagaaca<br>       <br> GAGGATCTCACGAATGC                   | gaacgaccggcacttga<br>  1<br>CTCGACGGAAAACCCAC                      | aagcggaaggto<br>                                       | tgcatcctaatcatgtt<br>                                              | ataacggttctgatatg<br>                                              | ctcactgtcttcgagtt<br>                                                 |
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1. .4647

/organism="Venturia inaequalis"

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/db_xref="texon:5025"

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/bondc(73. .261,318. .536,586. .2045,2094. .2848,2900. .4338)

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Cassette transporter ABC4 gene,
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Eukaryota: Fungi; Ascomycota; Pezizomycotina; Dothideomycetes
Chaetothyriomycetes incertae sedis; Venturiaceae; Venturia
                                               gaagccgaattatcagaag-agctttgtcaaggacgccttcccgcaaggccaatgctttg
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                                                                                                                                                                                                                                                                             5172 TCTGGCGGCCAAAAGCAACGTGTGGCCATTGCCCGAGCCCTTCTTCGGGATCCCAAAATC
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Schnabel, G., Schnabel, E.L. and Jones, A.L.
Complete sequences of four ABC transporters from Venturia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ATP-binding cassette transporter ABC4"
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Venturia inaequalis ATP-binding
complete cds.
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TITLE
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AUTHORS
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Pred. No. 3.5e-101;
1; Mismatches 1786;
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Best Local Similarity 47.7%;
Matches 1791; Conservative
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Fachin, A.L., Ferreira-Nozawa, M.S., Maccheroni, W. Jr. and Martinez-Fossi, M. M. M. Identification and Characterization of atrD gene, a new multidrug ATP-Binding Cassette Transporter of Trichophyton rubrum

(bases 1 to 4576)

Unpublished

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; Arthrodermataceae; mitosporic Arthrodermataceae;

(bases 1 to 4576)

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Pachin, A.L., Ferreira, Maccheroni, W. Jr. and Martinez-Rossi, N.M.
Direct Submission
Direct Submission
Direct Submitted (01-AUG-2000) Genetica, FMRP-USP, Ave: Bandeirantes 3900, Ribeirao Preto, SP 14049-900, Brazil
Gases I to 4576)
Fachin, A.L., Ferreira-Nozawa, M.S., Maccheroni, W. Jr. and Martinez-Rossi, N.M.
                                                                                                                                                                                                                                  Direct Submission
Submitted (09-AUG-2001) Genetica, FMRP-USP, Ave: Bandeirantes 3900,
Ribeirao Preto, SP 14049-900, Brazil
Sequence update by submitter
On Aug 9, 2001 this sequence version replaced g1:9885825.
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protein MDR

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<97. .>4144
/gene="atrD"
join(97. .438,491. .4144)
/gene="atrD"
/note="ABD transporter D"

1. 4576 /organism="Trichophyton rubrum" /db\_xref="taxon:5551" join(<97. .438,491. .>4144) /gene="atrD"

protein MDR

/codon\_start=1 /product="multidrug resistance

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Gaps
                                                                                                                                                      78;
                                                                                                                                             Length 4576;
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                                                                                                                                            10.3%; Score 392; DB 8; L
46.7%; Pred. No. 1.2e-98;
iive 1; Mismatches 1806;
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Matches 1653; Conservative
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ORIGIN
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4576 bp DNA linear PLN 10-AUG-20 complete cds. AF291822 AF291822 GI:15144501

2

DEFINITION

AF291822 LOCUS

ACCESSION

Trichophyton rubrum. Trichophyton rubrum

VERSION KEYWORDS SOURCE ORGANISM

10

| qq         | 583          | CCTCTACTTCGTCTATCTTGGAATCGCCCAATTATTCTCCTCTATGTATCCACTGTGGG 642             |
|------------|--------------|-----------------------------------------------------------------------------|
| oy<br>O    | 354          | cattaccatttcagctatacgaaccactcgaactcttcgacgagtgttccttgaatgcac 413<br>        |
| ογ         | 414          | 47                                                                          |
| <b>a</b> 8 | 703          | 76                                                                          |
| ž da       | 763          | cactaccaatggcaaccgtatacaaacaggtattgccgagaattggtctttaccgtgca 533<br>         |
| Oy<br>Ob   | 534          | ggcactttcaatgttctttctgcatttgtggtcgctttggcgtctcagtggaagctagc 593<br>         |
| à é        | 594          | tttaatoaccatgtccgtcatccctgccattttcctggtcaccggcatctgcatagcaat 653<br>        |
| oy d       | 654          | 71 71 10                                                                    |
| Qy         | 714          | 773                                                                         |
| Qy<br>Dp   | 774          | aaaatatgatgtctttttgcagcaagcaccaagaaggaag                                    |
| Qy<br>Dp   | 834          | tggsgtcttgttctcaactgagtacttttgcatttacgctgctatcgcactggccttttg 893<br>  :  :  |
| Oy<br>Dp   | 894<br>1183  | gaaaggttttegeatgtateagaatggegaggttgeegaegttggeaaagtetttaetgt 953<br>        |
| O.<br>Db   | 954          | tgtcctttccgtcaccttagcagccacgtccatctcaatgcttgcgccttcaggttcagt 1013           |
| Qy<br>Db   | 1014         | <pre>cgttaccaacgccgcatcttcggctccgaattattcagtatcattgacaaacccacgca 1073</pre> |
| Oy<br>Db   | 1074         | gctcgaccctctcgaaccttctggaaagcagcagagggctgcctaggtcaaattgagat 1133<br>        |
| da<br>Dp   | 1134         | ccaaaacctggcatttgcctacccctcccgaccatctgcccaagtacttcgagatttcaa 1193<br>       |
| Q Q        | 1194         | cttgacaattccagctggcaagacggccctcgtcggtggatcaggtagcggcaaaag 1253              |
| Oy<br>Dp   | 1254<br>1540 | cacaatggtcggcttacttgaacggtggtatctgccagttcggggaggagatattacttga 1313<br>      |
| Oy<br>Op   | 1314         | tgggttggaactgggacaatacaatgtgaaatggctgagaagccgcattcgcctcgttca 1373<br>       |
| QY<br>Dp   | 1374         | acaggaactgtgttgtttcgtggcacaatcttccagaacattgccaacggtttcatgga 1433<br>        |

2199 1911 aaaggcagcacgagaagctgctggtgaacgaccggcacttgagcgcactcacacccactgc 1970 2319 2120 2380 CACTITGATACGATTCATCGCTGGATTCAACAAGCCCGAGAGATTGATAATGCTCTGTGG 2439 2180 2499 2387 1551 cgagcgagccggagccttgagtggaggtcaacgacaacgaattgcaatcgcacgaagtat 1610 1900 TGTAAGCGACCCTAAGATATTATTGCTTGATGAAGCCACGTCTGCTCTGGAAACCGAAGTC 1959 tgcccacaaactagccactgtcaaaagtgctggcaacatcgcagtcatttcccaggggaa 1790 2020 CGCCCACCGTTTATCCACCATTAAATCTGCCGATAAATTTGTTGTGATTGTCGTGGTCG 2079 1851 ggtgcgtgcacaggacctcggggctgacgaacaacaagaacatgagaagaccctgcacga 1910 1971 cacatotoaagotagagacotagagaagoggaaggtgocggtogggacttggggotac-- 2028 2500 gggrancacaacantrogenecececearcattgraeggraaactgegegaagargeeaa 2559 2327 2388 totcacatogcaactgtcagctctacccacgcagttgcaagagttgatatcagcaaattt 2447 2740 ATTAACGTCATTCCTCTCAACTGAAACCAAGGATCTTCTGGGGTGGTGGTGCACTCT 2799 1434 tgagcaacgagatctgcctcgcgaaaaacaaat---ggagcttgtgcaaaaagcttgcaa 1490 1960 reaggergracraeccecrerreargergecreeccaggaagaacacrarrerear 2019 2200 CGAAAAGGAGAAGGAAATCTCGCGCCAGATTCTGTTCCTGCAAAGAGTGTCAACTCTGG 2259 -togotoctaaaatgcatcotaatcatgttotacgaacaaaaaatctotactggtgctt 2087 1720 GTCCCCAATGGAAAATGAATCCGAGGAGCAATCAAGGAACGGATCGTCAGTGCGGCCAA 1779 2260 AAAATACCCTGACGAAGATGTTGAAGCCAATCTTGGACGAATTGATACCAAGAAGTCCCT 2121 ggccacatttccaggacaagccctttgttttcgagattgctcactgtcttcgagttgag 2440 ATTCTTCTTTCTCTTTCTGGTGCTGGCCAGCCCGTTCAATCCGTCTTTTGCCAA tggctggacatgcaacgttatttcacaagttgtcacccatcgctatcaagccgcaatgtt 1611 catatoggatoccaagatoctgttactogatgaagotaccagogocottgacocgaaggo --ttctgatatgcgc ccaacgagtactggatcaagacatcgaactcctcgacatcccggagcaaatttctggtgc 1671 ggagaaagtggtccaggaggccttgaaccgagtgtccaaagaccgcactactttggtcat ---caggaacgggcaga CCGTGCAATGCTTCGACAAGATATTGCCTTCTTCGACCTCCCTGAGAACAGCACTGGTGC agecageaatggegaegtgtteattaatgagetteegaaeggttatgagaetgaagttgg cttgttgtcaacaataacgg-2181 tggtcatgcggca--1731 2029 2088 2268 2328 1491 셤 g g Q 0.y D.b q QY Db 9 P 9 2 2 QY Db QY Db Qγ Ω ŏ qq δ Qy Óγ Oy Db δ g οy g ò ò g ò

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KSVSSAVLSKVPEGPEKKYSLWTLVKRIGAFNRPELGYMLIGLTFSFLAGGGQPPQAF
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ARSQAFRSILEQDISFPDREBNSTGALISFLSTKNLGGVSGVTLGTINTSTTLGA
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IRTVASLTREODVWGVYHDQLQKQGRKSLISVLRSSLLYASSQALVFFCVALGFWYGG
TLLGHHEYSIFRFFVCFSEILFGAQSAGTVFSFAPDWGKAKNAAAQFKKLFDSKPTID
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Submitted (04-JUL-1996) Lilly Research Laboratories, Eli Lilly and
Company, Lilly Corporate Center, Indianapolis, IN 46285-0424, USA
Location/Qualifiers
1 5100
/organism="Aspergillus fumigatus"
/strain="loAF/86/10"
/db_xref="taxon:5085"
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itosporic Trichocomaceae; Aspergillus.
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224. .4417
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join(224. .610,693. .3997,4060. .4417)
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae;
1 (bases 1 to 5100)
Tobin, M.B., Peery, R.B. and Skatrud, P.L.
Genes encoding multiple drug resistance-like proteins
Aspergillus fumigatus and Aspergillus flavus
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Tobin, M.B.
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TTIALLERFYDALAGGVFVDGKDITKLNVNSYRSFLSIJVSQEPTLYQGTIKENILLGV
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2186 2058 geggecacatttecaggacaagecettttgtttteg-------agattgete 2163 TCAAGACCCGAAGTTACAGTCATGGAAGATGTCTCTTTATCGATGCCCGCGGGAAAGACT gtgaaatggctgagaagccgcattcgcctcgttcaacaggaacctgtgttgtttcgtggc acaatcttccagaacattgccaacggtttcatggatgagcaacgag---atctgcctcgc agtgctggcaacatcgcagtcatttcccaggggaaaatcgtcgagcaaggcacaccac gacgaacaacaagaacatgagaagaccctgcacgaaaaggcagcacgagaagctgctggt ATCGGTGCATTTAACCGCCCTGAGCTTGGTTACATGCTCATTGGCTTGACTTTCTCGTTC aagcagccagagggctgcctaggtcaaattgagatccaaaacctggcatttgcctacccc AAGGTACTCGACCATTTTGAAGGAAATATCGAATTTCGCAATGTCAAACACATCTACCCT acggccctcgtcggtgcatcaggtagcggcaaaagcacaatggtcggcttacttgaacgg CTCCGTTGGCTGCGACAGCAGATCTCTTGTCAGCCAGGAACCTGTTCTTTTCAGCACC gaaaaacaaatggagcttgtgcaaaaagcttgcaaagccagcaatggcgacgtgttcatt ACAGCCCACAACATTGTTGCCATGGTCGGCGGAAGATTGCCGAACAGGGAACATGAC GAGAAGGAAGCAGAAGCTCTGGAAGCCGACGCCGACATGGACGCCGATGATTTTGGTCAA gaacg----accggcacttgagcgcactcacaccactgccacatctcaa------GAAGGGGTTACTCGCATCAAGACTGCAGTTAGCAGCTCGAATTCTCTCGGTGCTGGTAGAT ----gctggagacctggagaagcggaaggtgccggtcgggactttggggctact GAGAAGGCGCCTTGGAGATGAAGCGAACCGGAACGCAAAAATCGGTTTCGAGTGCCGTT -----tqcatcctaatcatgttc tacgaacaaaaaaatctctactggtgcttcttgttgtcaacaataacggttctgatatgc tecegaecatetgeceaagtaettegagattteaaettgaeaatteeagetggeaagaeg cgctcctaaaa------1587 1159 1647 1707 1279 1767 1827 1947 1516 2007 1576 2067 2127 2187 1816 2307 2367 2427 2487 2547 1219 1339 1399 1456 1696 1876 1936 2119 1636 1981 ద Q D O.Y D.b 90 A2 O D Q Dp oy op 9. 0.y οp 0<u>7</u> δ В g q ŏ ò ò

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Peery, R.B. and Skatrud, P.L.
Multiple drug resistance gene of aspergillus flavus
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Location/Qualifiers
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Best Local Similarity 46.6%; Pred. No. 3.3e-90;
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/translation-*MKSDKDILMKPLPKSPGTGSTTTGHSVSHAEEVLDRQLHTPVSQ
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LKDAEGPGKKKSTAINVGALCIMFURGLGFWMGSRFVYGGIBSTLARKYESH
ATILGSYNLGNVAPNGQALSDAVAAASKLYGTIDRQSPLDALSDQGKTLEFVRGNIVL
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Aspergillus flavus
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Losses Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
Toblin,M.B., peery,R.B. and Skatrud,P.L.
Toblin,M.B., peery,R.B. and Skatrud,P.L.
Aspergillus fumliple drug resistance-like proteins in Aspergillus fumlgatus and Aspergillus flavus
Gene 200 (1-2), 11-23 (1997)
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Submitted (04-JUL-1996) Lilly Research Laboratories, Eli Lilly and
Company, Lilly Corporate Center, Indianapolis, IN 46285-0424, USA
Location/Qualifiers
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ga-agccgaattatcagaagagctttgtcaaggacgccttcccgcaaggccaatgctttg
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                                                                                            GGCAGCATTGGATGCCGCCGCGCGGGACACGACGATCGCAGTTGCTCACCGGCTGAG
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                                                                          gattttgtcatctctttaccagaaggctttgaaacgccttgcggctcaacgagggatgca
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/product="multdarug resistance protein
/protein.id="AAB88655.1"
/db_xref="GI:2673947"
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/strain="ATCC 24133"
/db_xref="taxon:5059"
1. 3924
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/gene="mdr1"
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Tobin, M.B.
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LDGHDICTALIALMARQMSLYSGEPRLEATTAENIRYGIIGSRERESFYEIRKKYE
AAARWANAHDFIMALDNGTVINIESFSLSGGQKORIAIARAIIKDPKILLIDEATSAL
DTKSEKLVQAALDKASKGRTTYJTAHRLSTIORAVIITVLANGOLYEGGBHEHLMDRR
GTYCDMVEAHEIKRYSKRYSKRYSOLTTVAHRLSTIORAVIITVLANGOLYEGGBHEHLMDRR
GTYCDMVEAHEIKRYSKRYSKRYSOLTTVAHRLSTIORAVIITVLANGOLYEGGBHEHLMDRR
DDASDIGGLIVGEKQRPVSRMSLSHLAMQPVEREANSFWILPKFLASFNRFEMPFLLLGI
CASILLAGGIQPSQAVLFARASGAFSTILLAGUSTVATLSAGTRELTGISG
VGTLEAYSSKWYTRARSQAFYVILHODISFEDQENTTGALTASGTREFORRAKK
AYOESASSACERASAIRTVASLGAAVSTURETBALQSYORGLRGOLLEGILVASGOLASGO
ALPFCMALGEWYGGSLIGGREYSLFOFYVCFSEVITGAQAGYFSHADDMGKARHA
AREFKRIFSSDTMHASRSGVPVYSIMETBALQSYORQLRGOLLEDILNILTIKPG
QFVALVGASGSGKSTTALLERRYDPLKGGYVUTGKNITTLEBESSYRSHLALISOEPT
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915 a 1018 c 1021 g 970 t

BASE COUNT 915 a 1018 c 1021 g 970 t
ORIGIN

14; 336 516 216 255 Gaps AAGAACTGGAAGCTGGCACTAATCTGTAGTGCCAGCCTGCTCGCATTGCTGTTGACCATG geogetgteetegeagaagaegtettateatecateeggaeagteeatgetttetaegee GAGATCACAACGAGGATCACCGCCGACACGAACCTGATTCAAGACGGTATCTCCCGAAAAG teteagtggaagetagetttaateaceatgteegteatecetgceatttteetggteace gactatctacgaatcttcagatatgccgacaaatacgactggactctcaatgtcatcgcg GGCTTTTTTGGTATCTATCGATATGCGACTCGATGGGATGTCGCCATTCTCTTCGGCAGT gtgttccttgaatgcaccttgcggcaagaggtctggcatttcgacaagcagagcaatgga ttggtctttaccgtgcacgtccatgttctttctgcattgtggtcgctttggcg Gregectagectreacegectreeacertegreacegectreateatana ggcatctgcatagcaattgatgccgctcaggaggccaggatcaccaggatctactcacgc GGTGGTTGCTCCACCCTCATGCTCATTTTAGCAAGAAAGCATTGGAATACCAGGGTCGT tacgitticcacggctgccattaccatttcagctatacgaaccactcgaactcttcgacga gcaatcgccactcargtcactaccaatggcaaccgtatacaaacaggtattgccgagaaa ttcaccaacaagttcaacaattacaattcgggcgacgggagtcctgaagcgttcaagggcc TTGACGTCGACCTTTCAAGACATCGCTACCCATCGGATTACGATCACTTCCATCAC TATCTAGCGACCGTCGGCTTCATTTATACCGGCGACCATGTCGTACAGCAGATTCGGGTG GAATACTICCAGGCIATCITAAGGCAGAATAITGCCITCITCGACACTCTIGGIGCIGGG Length 3924; Indels 9.5%; Score 362; DB 8; L 46.6%; Pred. No. 3.3e-90; Live 2; Mismatches 1892; Conservative Similarity Query Match Best Local Simi Matches 1752; 577 556 517 616 637 9/9 697 736 757 964 316 376 436 97 157 217 256 277 337 397 457 196 Oy Oy Oy Oy 용 07 07 08 08 08 g δ g Qy Db g ŏ g δ

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1470 1864 --acctcggggctgacgaacaacaagaacatgagaagaccctgcac 1908 agegeeettgaeeegaaggeggagaaagtggteeaggaggeettgaacegaatgteeaaa TCGGCCTTGGACAGGAAACCCGAAAAGCTCGGCGCTTGACAAGGCTTCTAAG GGTAGAACGACTATTGTCATCGCTCATCGCTGTCCACAATCCAGAAGGCATACAACATC gcagtcatttcccaggggaaaatcgtcgagcaaggcacaccaccgaattgatcgaattc ACTGTTGCCCATGATCTGAGTTGCTATATTCCTGCCGGTAAGACGACTGCCTTCGTGGGT GCGGGGACCATTATGCTCGACGGCCACGATATCCAGACATTGAATCTCCGATGGCTGCGA agccgcattcgcctcgttcaacaggaacctgtgttgtttcgtgggcacaatcttccagaac CAGCAAATGTCGCTCGTGTCGCAAGAGCCGAGACTCTTCGCCACCACCATCGGGGAGAAT cttgtgcaaaaagcttgcaaagccagcaatggcgacgtgttcattaatgagcttccgaac ggttatgagactgaagttggcgagcgagccggagccttgagtggaggtcaacgacaacga gaccgcactactttggtcattgcccacaaactagccactgtcaaaagtgctggcaacatc TATGGACTTGGCTTCTGGATGGGGTCTCGCTTCCTCGTCGAAGGAATCAGTAACATCAAA cttgcgccttcaggttcagtcgtttaccaacgccgcatcttcggctccgaattattcagt tgectaggtcaaattgagatccaaaacctggcatttgcctacccctcccgaccatctgcc caagtacttcgagatttcaacttgacaattccagctggcaagacggccctcgtcggt attgccaacggtttcatggatgagcaacgagatctgcctcgcgaaaaacaaat---ggag gttggcaaagtctttactgttgtcctttccgtcaccttagcagccacgtccatctaatg GTGGCCCCCAATGGACAAGCGCTGTCGGACGCTGTGGCGGCAGCATCAAAGCTGTATGGC atcattgacaaacccacgcagctcgaccctctcgacccttctggaaagcagccagagggc ategeactggecttttggaaaggttttegeatgtateagaatggegaggtt---geegae ggctgtcattacgccgcactggtgcgtgcacagg-------1690 1630 1750 1810 1870 1865 1054 1096 1114 1174 1216 1234 1276 1294 1354 1396 1414 1456 1471 1516 1531 1576 1591 1651 1711 1771 1831 856 916 994 64 G qq 9 QQ P Q OY Db δ g ò g ò g QY Db OY Db QΛ g ŏ qq Oy Db

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Filobasidiella neoformans multidrug resistance protein 1 (mdr1) mRNA, complete cds.
U62929.1 GI:2668552
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Heterobasidlomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
                                                                                                                                                      3177
                   3121 GACACAATGCATGCTTCTCGGAGCAAAGGAGTTCCGGTTACGTCCATGCGAGGACTGGTG 3180
                                                                                                   gacetegaggaeattgaatteaggtategteaaegtgatteggetegagtteteeggegg 3117
                                                                                                                                                                 TIGANCTGACCATCAAGCCAGGGCAATTGTTGCACTAGTGGGTGCGAGTGGAAGCGGC 3300
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acgagittiaccaaggeteggieggetgegaactatateetetggetgeggaeattgaag 2997
                                                                                                                           GAGTICCGCGATGICTCCTTTCGATATCCCAGTCGCTTGGAACAACCAATCCTTCGCCAC 3240
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                                                                                                                                                                                                                     tttgcacacgagaatattgcagaaatgtcgccgcgcttgtaccgcggccatatgtctttg
                                                                                                                                                                                                                                                                       3361 GTAGATGGAAAGATTATTATCACTCTCGAGATGTCTTCCTATCGCAGTCACTTGGCTCTC
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Thornewell,S.J., Peery,R.B. and Skatrud,P.L.
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                                                                                                                                    Direct Submission
Submitted (04-JUL-1996) Lilly Research Laboratories, Eli Lilly and
Company, Lilly Corporate Center, Indianapolis, IN 46285-0424, USA
Location/Qualifiers
                      CneMDR1: a Cryptococcus neoformans
to multidrug resistance proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ATP-binding cassette (ABC) transporter protein"
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                                                                                                                                                                                                                                                                                                                       /note="anamorph=Cryptococcus neoformans'
                                                                                                                                                                                                                                          neoformans
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Pred. No. 3.6e-87;
1; Mismatches 1829;
                                                                                                                                                                                                                                        /organism="Filobasidiella
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Best Local Similarity 46.5%;
Matches 1661; Conservative
                                                                                               2 (bases 1 to 4227)
Skatrud, P.L.
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                                              874 GGAACATCTGAAAAGGTCGCTCTCGTATTCCAATATGCTGGTACTTTTGTCTGCGGTTTT
                                                                                                                                              934 GTTCTAGCTTTTGTCCGGTCACCTCGTCTTGCGGGGCGCTCTTGTTTCCATCCTGCCAGTC
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| 1638<br>2010<br>1698<br>2070<br>1758<br>2130                 | 1818<br>2190<br>1875<br>2250                             | 31<br>31<br>37                  | 2055                                                             | 2115                                                        | 2129           | 2187<br>2610                                                  | 2244                                                          | 2304                                                             | 2364                                                         | 2424                                                         | 2482                                                       | 2542<br>2967                                                   | 2602<br>3027                                                | 2662                                                         |
|--------------------------------------------------------------|----------------------------------------------------------|---------------------------------|------------------------------------------------------------------|-------------------------------------------------------------|----------------|---------------------------------------------------------------|---------------------------------------------------------------|------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|
| caacgacaacgaattgcaatcgcacgaagtatcatatcggatcccaggatcctgttactc | gctggcaacatcgcagtcatttcccaggggaaaatcgtcgagcaaggaacacacac | gac<br> - <br>GAA<br>gaa<br>TTC | aagcggaaggtgccggtcgggactttgggctactcgctcctaaaatgcatcctaatcatg<br> | ttctacgaacaaaaaatctctactggtgcttcttgttgtcaacaataacggttctgata | tgcgcggcacatt  | tccaggacaagccttttgttttcgagattgctcactgtcttcgagttgagtggtcat<br> | geggcacaggaacgggcagacttttatattctgatgttctttgtcgtggctctagga<br> | aatctagtaggatatttcacgattggctggacatgcaacgttatttcacaagttgtcacc<br> | catcgctatcaagccgcaatgttccaacgagtactggatcaagacatcgaactcctcgac | atcccggagcaaatttctggtgctctcacatcgcaactgtcagctctacccacgcagttg | caagagttgatatcagcaaattttctcatttatatcgttgtcggtcaacatcgtctcg | agcagtgctctaccactagcctatggatggaaactgggcctggtggttgtttggtgca<br> | cttccaccctgcttttggctgctacctcagaattcgtctagagacgaagcccigiliii | ggaaactcggcaaactttgcagaaagtgctgggcttgcaagcgaagcagttaccgcgatc |
| 1579<br>1951<br>1639<br>2011<br>1699<br>2071                 | 1759<br>2131<br>1819<br>2191                             | 87<br>25<br>93                  | 1996<br>2371                                                     | 2056                                                        | 2116           | 2130                                                          | 2188                                                          | 2245                                                             | 2305                                                         | 2365<br>2791                                                 | 2425<br>2851                                               | 2483<br>2911                                                   | 2543<br>2968                                                | 2603                                                         |
| Oy<br>Oy<br>Oy<br>Oy                                         | 70 da da                                                 | oy<br>Oy                        | oy<br>op                                                         | 0y<br>0p                                                    | ζ <sub>δ</sub> | Qy<br>Dp                                                      | O.Y                                                           | 9 64<br>19 64                                                    | 0.4<br>0.4                                                   | Qy                                                           | Oy<br>Dp                                                   | oy<br>Dp                                                       | Oy<br>Db                                                    | οy                                                           |

2722 agcaaggictigctaagaicaiccaaagciiitiggiiigaagaigiiiiggiiiticaci 2782 2901 3325 3608 2961 3315 3564 3196 tigicggaacgattctacgacccgacctcgggccgaatttcatttgcacacgagaatatt 3255 3684 3744 tgaggcatccacgagccgaacgacaatagcagtggcgcaccgacttccactattcggaa 3668 tgttgatgttatttttgtgttttgccaacgggagaatcgccgaaacgggcactcacgcggga 3728 -cercratreaageresaarstererectrescescessasses 3385 TCGGCCGCCTCCATCTTCCGAAGCATCGACAATGAACCGGCTATCAATGCAATCTAAT 3444 3445 GAAGGGAAGGTGCTTGATCACAAGCACGTCGTTGGTCATGTGCGAATTGAAGGCGTTCAC 3504 3136 ccaggacaatttgtagcttatgtgggcgcttctggctgtggcaagtcaacgttgatcgct 3195 ctttaccaaggetecgttegegagaatgtgaegttggeeetegaageegaattateagaa 3375 3745 CTTTACGCGGGTACAATTAGGTTTAATATTCTTTTGGGCGCGAACAAGCCCATAGAGGAG 3804 3805 GTGACTCAGGATGAGATTGATGCTGCCTGCAAGGATGCCAATATTTACGACTTTATCGTG 3864 3924 TCAAAAGCAACGTATCGCTATCGCCCGTGCTCTCATTCGAAACCCTAAAGTCTTGCTCT 3983 TGACGAAGCTACGTCCGCACTCGACAGTCAGTCAGAAAAGGTCGTTCAGGAGGCACTTGA 4043 2783 tgtcacagtcgatggagtttttggctattgcctgggattttgtatt-gcagtcgataat 3088 AAGACAGTAGCCAGTCTTACCAGGGAGGATGTAAGGAGAATCTATTCTGAAGCTCTT 3266 TCATCGATGCCAATACTCCACTGCTAGTTTCTATACTGTCTTGAACTCCATTGTCTTTG gctgcgaactatatcctctggctgcggacattgaagccgaccatccgcga----aacg gaggagaacaagaaaaaaggcccagtgggtggatgccttgtcgacctcgaggacattgaa 3256 gcagaaatgtcgccgcgcttgtaccgcggccatatgtctttggtccaacaggaaccacaca 3685 AAGGAGCTCAACTTGGCGAGTTACCGTAGCCAGATCTCCCTCGTTTCTCAAGAACCTACC gcaacgacagcggatcgccatcgcaagagcattgattcgaaatccaaagctgttgctact cggaccgtctcatctttgactctcgaaggccatgttctccaacagtactcggacatgttg A - - AAGCTCCTATGAAATTAAATTTCCGTACTTCTATTAAATCCCAGTGTCTCTTTGCGG coggiccaagcagcagcagtattiggcitaciccacgagtittaccaaggcicggicg ttcaggtatcgtcaacgtgattcggctcgagttctccgcgggggtttccatgacaatcgag 3565 GCCGCCACTTATGTGGCACTCGTTGGTCGTTGTGGAAAGTCTACCACTATTCAA tgacgaagcgacgtcagccctcgacacgcaatcggaacgtctggttcaagctgccctcga 3076 2663 2723 3148 2842 2902 3326 2962 3016 3316 3376 3549 3489 3984 3609 4044 3669 셤 ò 셤 ò g ò 셤 ò q ò g ò g ò q ð q q g ογ g q g g ò ò ò à ò ð 셤 ò g 8 ò ò

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Expression of atrC-encoding a novel member of the ATP binding cassette transporter family in Aspergillus nidulans-is sensitive to
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GYLITVLTSVLIGSQSLTLIGPFIGEVSKTAAAAQELFQVIDRKPNIDSLSSDGRTUT
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AMLNQDVSFFEEEDQSAGTWTGOLSTDPRIEDLISLCLGFILLVVVNVLASCILALA
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LTLIVVAATLEPHIVKAYNADLVSHYLIGTRITKILAIYSKAGGIAEEALASTHIVKAYNAAS
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LTLEEKVIQMYDERLSHTSPKFIRITLVSAILLGLCESLYLATLGLIFWYGVKLLSOG
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ETVQLDSDTALEFKDVHFSYPARPTVPVLQGLSFKVKKGEHIGLVGASGCGKTTVISL
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NEELDSQIEERLTKAYKDANIQDFIQSLPEGQQTDPGTRGLALSGGGRQRIAIARALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-AUG-1998) Institut fuer Mikrobiologie Medizinische Fakultaet, Universitaet Innsbruck, Fritz-Pregl-Str. 3, Innsbruck
4104 TTCTGACCGGATTTACTACTTCTCTGAAGGCAGGGTAGCCGAGCATGGAACACATCAGGA 4163
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 4872)
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Biochim. Biophys. Acta 1453 (2), 304-310 (1999)
99156773
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/qene="atrC"
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                                    3729 actacaacgactgagaggaagatattacgagatg 3762
                                                                  2 (bases 1 to 4872)
Angermayr,K., Parson,W. and Haas,H.
Direct Submission
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FEATURES

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                                                                                                                                                                                                                                                                                                                   685 AGCTIAITITCGAGTCTGGGGGTÁCTCGAGCGTCCAGGATCATGTGATCAGGGTCACTGG 744
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46.2%; Pred. No. 7.5e-85;
tive 1; Mismatches 1901;
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3719 ctcacgcggaactacaacgactgagaggaagatattacgagatgtgtttggcacaatctt 3778 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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Search completed: April 26, 2002, 23:14:16 Job time: 13845 sec

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APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
APPLICANT: de Waard, Maarten A.
APPLICANT: Peery, Robert B.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
CORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,545
CIASATEMATE.
                                            US-08-044-812A-3
US-08-475-837-3
US-08-191-359-3
US-09-191-359-3
US-08-752-929-18
US-08-752-929-18
US-08-216-971-1
US-08-216-971-1
US-08-868-435-3
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PCT-US93-06251-83
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US-08-982-412-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREE: Eli Lilly and Company STREE: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         x-11766
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08996545
Patent No. 5928898
GENERAL INFORMATION:
SAPELICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-117
FELECHONICATION INFORMATION:
TELEPHONE: 317-276-334
TELEPAX: 317-276-3334
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
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LOCATION:
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FEATURE:
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Sequence 5, Appl
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-479-744A-32
US-08-280-757B-32
US-08-740-309-1
US-08-286-889-45
US-08-485-618-45
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US-08-605-672-45
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-09-522-494-55
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S-08-485-618-52
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                                                                                                                                                                                                                                                                                                           383533 seqs, 122816752 residues
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                                                                                                                  April 27, 2002, 05:55:15
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Gapop 60.0 , Gapext 60.0
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0.6%; Score 21; DB 2; Length 4002;
100.0%; Pred. No. 0.8;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                            Sequence 3, Application US/08996545
Patent No. 5928898
GENERAL INFORMATION:
APPLICANT: Skatud, Paul L.
APPLICANT: Peery, Robert B.
APPLICANT: Peery, Robert B.
APPLICANT: Peery, Robert B.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 21; DB 2; Length 4002; 90.5%; Pred. No. 0.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11766
TELECOMMUNICATION INFORMATION:
TELEFAX: 317-276-2763
INFORMATION FOR SEQ ID NO: 35.
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATANTION Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/996,545
                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09328320; Patent No. 6228615; GENERAL INFORMATION: APPLICANT: SKatrud, Paul L. APPLICANT: Peery, Robert B.
                                                                            3553 gaagegaegteageectegae 3573
                                                                                                   3763 GAAGCGACGTCAGCCCTCGAC 3783
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                  Best Local Similarity 100. Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Lilly Corpor CITY: Indianapolis STATE: Indiana COUNTRY: U.S. ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
US-08-996-545-3
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US-08-996-545-3
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US-09-328-320-1
  Query Match
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APPLICANT: Skatrud, Paul L.
APPLICANT: de Waard, Maarten A.
APPLICANT: Derry, Robert B.
APPLICANT: Andrade, Alan C.
TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of TITLE OF INVENTION: Aspergillus Nidulans
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: 11 Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4002;
               Multiple Drug Resistance Gene atrD of Aspergillus Nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indianapolis
COUNTRY: U.S.
ZIP: 46285
COUNTRY: U.S.
ZIP: 46285
COUNTRY: IBM PC COMPALIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
CONTRARE: PatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/328,320
FILING DATE:
APPLICATION NUMBER: US/09/328,320
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: 39,872
REFERENCE/DOCKET NUMBER: 3,7176
TELEPHONE: 317-276-3334
TELEFAX: 317-276-3334
TELEFAX: 317-276-3334
TELEFAX: 317-276-3334
TELEFAX: 317-276-3334
TELEFAX: 317-276-3334
TELEFAX: SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Ilnear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 0.6%; Score 21; DB 4; Best Local Similarity 100.0%; Pred. No. 0.8; Matches 21; Conservative 0; Mismatches
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US-09-288-320-3
; Sequence 3, Application US/09328320
; Patent No. 6228615
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Andrade, Alan C.
                 TITLE OF INVENTION: MU
TITLE OF INVENTION: AS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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Sequence 32, Application US/08280757B

Patent No. 6130316

GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
TITLE OF INVENTION: S.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEN FC Compatible
COMPUTER: TEN FC COMPATIBLE
COMPUTER: THE MC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/10,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/10,773
FILING DATE: 3-AUG-1993
APPLICATION NUMBER: 08/10,773
FILING DATE: 3-NOV-1993
ATTOMETY AND NUMBER: 08/10,773
FILING DATE: 3-NOV-1993
ATTOMETY AND NUMBER: 08/10,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 3;
Pred. No. 28;
0; Mismatches
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 227-7400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACIERISTICS:
                APLICATION NUMBER: 08/147,773
APLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTONEY FACENT INFORMATION:
NAME: MANDERS AMY E.
REGISTRATION NUMBER: 36,207
REPERBENCE/DOCKET NUMBER: RPI-004CP3
FELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Sc
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: oligonucleotide US-08-479-744A-32
    26-JULY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1974 atctcaagctggagacct 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ATCTCAAGCTGGAGACCT 7
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US-08-280-757B-32/c
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US-08-479-744A-32/C
Sequence 32, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Gray, Gary, Gary
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
MUMBER FO FSQUENCES: 55
CORRESPONDENCES: 55
STREET: 60 State Street
Tare Of State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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90.5%; Pred. No. 0.8;
tive 2; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/328,320
FILING DATE:
                                                                                                                                                                                                                                                                                                    NAME: Webster, Thomas D.
RECISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11766
TELEPHONE: 317-276-3334
TELEPAX: 317-276-2763
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,545
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APPLICATION NUMBER: 08/101,624
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                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.59
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
US-09-328-320-3
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Gaps

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1281 CGCACTGGCCTTTTGGAA 1298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 52..3519
US-08-286-889-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA FEATURE:
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US-08-485-618-45
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Petent No. 5470953
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STRRET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                        US-08-140/309-1
US-08-740/309-1
US-08-740/309-1
Sequence 1, Application US/08740309
Sequence 1, Application US/08740309
Sequence 1, Application US/08740309
Sequence 1, Application US/08740309
SEQUENCE 1 INFORMATION:
WUMBER OF SEQUENCES: 3
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SPETANES: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
                                                                                                                                                                                   Query Match 0.5%; Score 18; DB 3; Length 39; Best Local Similarity 100.0%; Pred. No. 28; Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 27;
tve 0; Mismatches
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APPLICATION NUMBER: GB 9408344.1
FILING DATE: 27-APR-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-280-7578-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Sc
Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-740-309-1
                                                                                                                                                                                                                                                                            1974 atctcaagctggagacct 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1568 tgagtggaggtcaacgac 1585
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                                                                                                                                                                                                                                                                                                          24 ATCTCAAGCTGGAGACCT 7
LENGTH: 39 base pairs
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US-08-286-889-45
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Sequence 45, Application US/08485618
Fatent No. 5728533
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, Wondca
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 66606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION THE TO SET THE SET TO SET THE SET TO SET THE SET TO SE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PACENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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Pred. No. 27;
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Db 1281 CGCACTGGCCTTTTGGAA 1298
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                    Query Match 0.5%
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATERISTICS:
             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
52..3519
                                                                                                                                               52..3519
                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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MOLECULE TYPE:
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                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-362-652-45
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; LOCATION:
US-08-605-672-45
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Patent No. 5766850
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTIONS: 93
CORRESPONDENCE 93
CORRESPONDENCE ADDRESS:
ADDRESSE: MARSHALL, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
Illinois
COMPUTER: Enhande FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CHERENT APPLICATION NUMBER: US/08/362,652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
FILING DATE: 21-DEC-1994
ATORNEY AGENT INFORMATION:
MAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELECHONE: 312-474-6300
TELERAX: 312-474-6300
TELERAX: 312-474-6448
TELERAX: 312-474-6418
TELERAX: 313-474-6418
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659

RECISTRATION NUMBER: 38,659

RELEPHONE: 312-474-6300

TELEPHONE: 312-474-6300

TELEPHONE: 312-474-6300

TELEPHONE: 312-474-6300

TELEPRAX: 25-3856

INFORMATION FOR SEQ ID NO: 45:
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52..3519
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 18; Conserv
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; LOCATION:
US-08-485-618-45
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STRANDEDNESS: single

TOPOLOGY: linear

WOLCOGY: 32.319

US-09-56-563-45

US-09-56-563-46

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Sequence 45, Application US/08943363
Sequence 45, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                            STREET: 233 SOUTH WACKET DITUE, 0300 SEAL LOWER CITY: 111nois COUNTRY: United States COMPUTER: 111nois COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Plappy disk COMPUTER: Patentin PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NOMBER: US/08/943,363 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 18; DB 2;
100.0%; Pred. No. 27;
11ve 0; Mismatches
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Sequence 45. Application US/09193043
Patent No. 6251305
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATFORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 27866/32684
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27866/32684
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INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1281 CGCACTGGCCTTTTGGAA 1298
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Matches 18; Conservative
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), LOCATION: 52..3519
US-08-943-363-45
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                       US-08-943-363-45
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                                               Gaps
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APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
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red. No. 27;
Mismatches 0; Indels
DB 1; Length 3519;
27;
                                               0; Indels
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0.5%; Score 18; DB 100.0%; Pred. No. 27; Lve 0; Mismatches
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CLASSIFICATION NUMBER: US/US/402,233A
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/13,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGGNT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
RECISTRATION NUMBER: 38,659
RECISTRATION NUMBER: 38,659
TELECOMMUNICATION NUMBER: 27866/32684
TELECOMMUNICATION NUMBER: 27866/32684
TELECOMMUNICATION NUMBER: 27866/32684
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NS-08-482.293A-45
Sequence 45, Application US/08482293A
Patent No. 5831029
    0.5%,
100.0%; Pre
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 3519 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1281 CGCACTGGCCTTTTGGAA 1298
                                                                                          879 cgcactggccttttggaa 896
Ouery Match 0.5%
Best Local Similarity 100.C
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 52..
US-08-482-293A-45
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| Patent No. 5728533
| GENERAL INFORMATION: APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit NUMBER OF SEQUENCES: 103
| CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-193-043-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.5%; Score 18; DB 4; Length 3519; Best Local Similarity 100.0%; Pred. No. 27; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUDIESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STRRET: 233 South Wacker Drive, 6300 Sear Tower CTTY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE: US/08/485,618
FILING DATE: US/08/485,618
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: S-AUG-1994
PRIOR APPLICATION NUMBER: US 08/286,889
FILING DATE: S-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
PRIOR APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT: 1NFORMATION:
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER: OF SEQ ID NOS: 114
SOFTWARE: PATENTIN NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 45
LENGTH: 3519
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REFERENCE/DOCKET NUMBER: 7866/32797
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 cgcactggccttttggaa 896
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COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (52)..(3516)
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-485-618-52
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| TELEPHONE: 312-474-6300 |
| TELEPHONE: 312-474-6300 |
| TELEFA: 312-474-0448 |
| TELEX: 25-3856 |
| TELEX: 25-3856 |
| TELEX: 25-3856 |
| INFORMATION FOR SEQ ID NO: 52: |
| SEQUENCE CHARACTERISTICS: |
| LENGTH: 3803 base pairs |
| TYPE: nucleic acid |
| TAPE: nucleic acid
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em\_esthum:\* em\_estin:\* em\_estmu:\* em\_estov:\* em\_estpl:\*

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Database

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Searched:

Minimum DB Maximum DB

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o52c01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1053504 5' similar to gb:s60080 DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases i to 327) and ito 327, Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The Wash, HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/db_xref="taxon:10090"
/dclone="IMAGE:1053504"
/clone="Ib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH108"
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Contact: Marra MyMouse EST Project
Contact: Marna MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porcest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 21; DB 9; Length 325; 100.0%; Pred. No. 27; tive 0; Mismatches 0; Indels
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Seg primer: -28m13 rev2 ET from Amersham.
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            /lab_host-"DH10B"
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                                                                                  /dow_stage="Adult plant"
//dow_stage="Adult plant"
//dow_stage="Adult plant"
//dow_stage="Adult plant"
//dow_stage="WetCor: Lambda Uni-ZAP XR, excised phagemid
//down in the greenhouse. Spikes were sprayed at anthesis
grown in the greenhouse. Spikes were sprayed at anthesis
with Fusarium graminearum. Total RNA, and poly(A) RNA were
prepared and pooled from infected spike at 0, 6, 12, 24,
36 and 48 hours after incoulation, a cDNA library was made
, and the cDNA clones were in vivo excised to give
pBluescript phagemids in G. Muchlbauer lab at the
University of Minnesota (Kurger, W.M., Muchlbauer, G.J.,
Pritsch, C., Vance, C.). The cDNA library should contain
genes of both wheat and fungal pathogen origin. Plasmid
DNA preparations and DNA sequencing were performed in the
OD Anderson lab (all other authors)."
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/clone_lib="Wheat Fusarium graminearum infected spike cDNA
library"
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R. (ardenas, M., McCann, R., Materston, R. and Wilson, R.)
The Washlo-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.linl.gov) for further information. MGI:585080
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="InAGE:1053504"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
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    .325
    /organism="Mus musculus"

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100.0%; Pred. No.
ative 0; Mismatch
                                                                   /tissue_type="Spike"
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Akimura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T. Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tayanishi, F., Takaku-Akahira, S., Matahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
T 3/]; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library constructed by Bob Barstead. *
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UKL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayasu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Huramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/organism="Mus musculus"

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FEATURES

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BB670723 RIKEN full-length enriched, 10 days embryo Mus musculus CBN C507723 RIKEN full-length enriched, 10 days embryo Mus musculus CBNA clone 342540HH16 3', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Faxi: 81-15-1000 Faxi: Yokohama, Kanagawa 230-0045, Japan
WRL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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                                                                                                               /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was
                                       /clone_lib="RIKEN full-length enriched, 10 days embryo"
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/lab_host="DH10B"
/db_xref="taxon:10090"
/clone="3425401B20"
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Contact: Yoshihide Hayashizaki
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house mouse.
                                                                                                                  Unpublished (2001)
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
As, Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Konno,H., Pukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y., and Hayashizaki,Y.
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Manmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 359)
Akimura,T., Arakawa; T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB803996 RIKEN full-length enriched, 10 days pregnant adult female ovary and uterus Mus musculus cDNA clone G630061C01 3', mRNA
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                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                 1. .343
/organism="Nus musculus"
/strain="C57BL/65"
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/clone="3425401H16"
/clone="1b="RIKEN full-length enriched, 10 days embryo"
/dev_stage="10 days embryo"
/lab_host="DH10B"
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Matches 21; Conservative
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FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-171 (2000) For the multicapillary sequencer. Genome Res. . Xonno.H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) further details.
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AU020440 Mouse eight-cell stage embryo cDNA Mus musculus cDNA clone
AU020440
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Yomaru, A., Toya, T., Watchiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Rikon Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL: http://genome.gsc.riken.go.jp,
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9222
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 386)
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/dLxref="taxon:10090"
/clone="G53006LC01"
/clone_lib="RiKEN full-length enriched, 10 days pregnant adult female ovary and uterus"
/sex="female"
/tissue_type="ovary and uterus"
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101 c 73 g 78 t
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100.0%; Pred. No. 27;
tve 0; Mismatches
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Matches 21; Conservative 0;
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POLYA=Yes.
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KO,M.S.H, Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R. and Doi,H. Systematic analyses of genes expressed in eight-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko M.S.H. et al.)
Unpublished (1998)
Contact: Hirofumi Doi
Doi Bioasymmetry, Project, ERATO
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The sequence contained an oilgo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to identify it as a clone from the normalized atrium at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seg priner: MI3 Forward
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                      Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebiast 190.jp.
Location/Qualifiers
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UI-R-BJ1-aws-g-12-0-UI.sl UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-aws-g-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse eight-cell stage embryo cDNA"
/dev_stage="eight-cell stage embryo"
80 c 107 g 115 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 21; DB 9; Length 386; 100.0%; Pred. No. 28; Live 0; Mismatches 0; Indels
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Program for Rat Gene Discovery and Mapping
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/db_xref="taxon:10116"

    .386
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
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/clone_ib__rulr. Bars_s_s_rulr. Clone_ib__rulr. Bars_s_s_rulr. Rednologies)"
/lab_host="Vector: pr713D-pec (Pharmacia) with a modified fnote="vector: pr713D-pec (Pharmacia) with a modified polylinker; Site_l: Not i; Site_2: Ecc RI; The UI-R-BJI library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, ventricle at 13 dpc, and adult heart. Av canal at 15 dpc, ventricle at 15 dpc, ventricle at 15 dpc, ventricle at 15 dpc, rednologe, ventricle at 15 dpc, ventricle at 15 dpc, retricle at 15
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 399)
Plao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Luo, A. and
Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI: Site_2: NotI: Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Contact: Dawood B. Dudekula
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/clone=lib="Na Mouse Blastocyst cDNA Library (Long)"
/tissue_type="Blastocyst"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
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National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C083 I row: B column: 02
Seg primer: -21M13 Forward
High quality sequence stop: 399
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/clone="UI-R-BJ1-aws-g-12-0-UI"
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/db_xref="niaEST:C0833B02-3"
/db_xref="taxon:10090"
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1. 399
/organism="Mus musculus"
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Best Local Similarity 100.
Matches 21; Conservative
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TITLE
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                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 402)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiranoto,K., Hiraoka,T., Imorani,K., Ishii, Y., Ito,M., Kawai,J., Nomiura,K., Nonno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomiura,K., Numsaski,R., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Shiraki,T., Sogabe,T., Tomaru,A., Tagawa,A., Shiraki,T., Sogabe,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suebliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
extracted from a pool of 20 Blastocysts. Double-stranded CDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB735228 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F420015G18 3', mRNA sequence.
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100.0%; Pred. No. 28;
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BB735228.1 GI:16134378
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Best Local Similarity
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Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
Program for Rat Gene Discovery and Mapping
University of Lowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8256
Email: macaresebblue.weeg.uiowa.edu
The sequence contained an oilgo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA Library Preparation: M.B. Soares Lab Clone distribution: CDNA Library Preparation: M.B. Soares Lab Clone distribution: This clone is also available through Research Genetics (www.resgen.com)
LLNL (info@image.llnl.gov). IMAGE ID=1785641
Seq primer: Ml3 Forward
POLYA=NO.
sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone=FF420015G18"
/clone_lib="RKEN full-length enriched, 6 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="spleen"
/dev_stage="6 days neonate"
111 c 84 g 88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.6%; Score 21; DB 98st Local Similarity 100.0%; Pred. No. 28; Matches 21; Conservative 0; Mismatches
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                     e mouse tissues.
Location/Qualifiers
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DEFINITION
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                   /deb_stage="DH10B (Life Technologies)"
/dab_host="DH10B (Life Technologies)"
/dab_stage="DH10B (Life Technologies)"
/dote="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: ECO RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from an placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of CDNAs from which ESTS had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1,
// UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3.5
nucleotides present between the Not I site and the
oligo-dr track whichallows identification of the library
of origin of a clone within themixture. The subtracted
library (UI-R-C3) was constructed as follows: PCRampilified
congin of a clone within themixture in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxypafite column
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Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanakashi, F., Takaku-Akahira, S., Tanakaki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB672487 RIKEN full-length enriched, adult male brain Mus musculus cDNA alone 3526405D03 3', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-rho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UI-RC3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)*
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100.0%; Pred. No. 28;
tive 0; Mismatches
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Contact: Yoshihide Hayashizaki
/dev_stage="adult"
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Best Local Similarity 100.
Matches 21; Conservative
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BB672487
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' and adapter of sequence [5' and adapter of sequence [7' as a constant of the transcript and bamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnindt.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch
Carnindt.p., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
pepare full-length CDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Natahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anote—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RREN" full-length enriched, adult male brain"
/sex="male"
/rssue_type="brain"
/dev_stage="adult"
/lab_host="BH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 28;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3526405D03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e mouse tissues.
Location/Qualifiers
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us-09-882-694a-10.rst

REFERENCE AUTHORS JOURNAL COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Sciurognathi; Murinae; Mus.; 1 (bases 1 to 430)

S. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Tumor Gene Index

Nutional Cancer Institute, Ph.D.
Email: capabbers-femalinh.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:637374
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 296.
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Bukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Buteleostomi;

Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 432)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatau,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishli

Y., Ito,M., Kawal,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Salto,R., Sakal,C., Sakal,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

87 c 116 g 130 t 2 others
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BB670914 RIKEN full-length enriched, 10 days embryo Mus musculus
CDNA clone 3425403B19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 21; DB 9; Length 430;
100.0%; Pred. No. 28;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1179526"
/clone_ib="Soares_mammary_gland_NbMMG"
/sex="male"
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/lab_host="DH10B"
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Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                               AL Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-reségsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,Y.
Normalization and subfraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Taawa,M., Ohara,E.,
Watahiki,M., Yokazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizati,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 177-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                         1 (bases 1 to 404)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatau,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Hayatau,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Watsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibate,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
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   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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A1643840.1 G1:4722315
EST.
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/cell_line="RCB-0558 LLC"
109 c 82 9 94
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BASE COUNT

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Lupublished (2001)

Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan
Tel: 81-45-503-9212
Email: genome-rese@sc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Wayaiki.Y. Shibakay.Y. Togawa,Y. Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y. Ishikawaj.T. Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
Sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
V and Hayashizaki,V. Shibata,K., Itoh,M., Carninci,P., Sugahara
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, Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/60"
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/clone="3428403B19"
/clone_lib="RIKEN full-length enriched, 10 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......, v., and Hayashizaki, v., subbata, n., tton, m., carninci, p., Sugah v. and Hayashizaki, t. and hayashizaki, t. and hayashizaki, so computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/lab_host="DH108"
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                                      TITLE
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Search completed: April 27, 2002, 02:59:00 Job time: 13452 sec

0.6%; Score 21; DB 9; Length 432; 100.0%; Pred. No. 28; tive 0; Mismatches 0; Indels 1401 aatcttccagaacattgccaa 1421 ολ

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Query Match

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7777, A 4093, A 21907,

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; Search time 95.74 Seconds
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7275.887 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq length: 200000000
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Perfect score:
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Post-processing: Listing first 45 summaries

Pending\_Patents\_NA\_New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 23868, A sequence 31943, A sequence 13179, A sequence 109, App Sequence 11641, A Sequence 11641, A Sequence 26, Appl Sequence 26, Appl Sequence 6764, App Sequence 6764, App Sequence 6769, App Sequence 64, Appl Sequence 346, Appl Sequence 3146, Appl Sequence 1791, Appl Sequence 1791, Appl Sequence 346, Appl Sequence 346, Appl Sequence 1784, Appl Sequence 501, Appl Sequence 1784, Appl Sequence 1784, Appl Sequence 1784, Appl Sequence 501, Appl Sequence 1784, Appl Sequence 105, Appl Sequence 105, Appl Sequence 106,
SUMMARIES	US-09-540-210B-23868 US-09-540-210B-31943 US-09-540-210B-9536 US-10-115-123-109 US-10-115-123-109 US-10-115-123-100 US-10-115-123-100 US-10-115-123-100 US-10-115-123-100 US-10-115-129-6764 US-10-105-299-6768 US-10-105-299-6768 US-10-105-299-6768 US-10-105-299-6768 US-10-105-299-6768 US-09-540-210B-34467 US-09-540-210B-34467 US-09-540-210B-34467 US-09-540-210B-34467 US-09-540-210B-348-903 US-09-540-210B-348-903 US-09-540-210B-348-903 US-09-540-210B-348-903 US-09-540-210B-348-903 US-09-540-20B-346 US-10-105-299-7324 US-10-105-299-7324 US-10-101-588-14
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% Query Match Length	251 271 276 276 276 276 276 276 276 277 277 277
% Query Match	00000000000000000000000000000000000000
Score	10000000000000000000000000000000000000
Result No.	00000000000000000000000000000000000000

RESULT  US-09-540-210B-23868/C Sequence 23868, Appl GENERAL INFORMATION: APPLICANT: Sellhame APPLICANT: Stuart, APPLICANT: Stuart, APPLICANT: Stuart, APPLICANT: Mullahy APPLICATION N FRICK FILLING DATE: PRIOR FILLING DATE: PRIOR FILLING DATE: PRIOR FILLING DATE: PRIOR APPLICATION N PRIOR FILLING DATE:
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APPLICANT: Sellahmer, Jeffrey J.
APPLICANT: Sellahmer, Jaffrey J.
APPLICANT: Sellahmer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE FILE REFERENCE: PD-1037 CIP
CURRENT APPLICATION NUMBER: US/09/540,210B
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 08/972,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR PELLICATION NUMBER: 09/05/2007 OR PELLING DATE: September 29, 1995 OR APPLICATION NUMBER: 08/824 029 OR FILING DATE: March 25, 1997 OR FILING DATE: March 25, 1996 OR APPLICATION NUMBER: 06/015, 1996 OR APPLICATION NUMBER: 06/015, 533 OR FILING DATE: APR'11 10, 1997 OR APPLICATION NUMBER: 06/015, 533 OR FILING DATE: July 31, 1996 OR APPLICATION NUMBER: 06/013, 308 OR FILING DATE: July 31, 1996 OR APPLICATION NUMBER: 08/862,178 OR FILING DATE: May 22, 1997 OR APPLICATION NUMBER: 08/862,178 OR FILING DATE: May 23, 1996 OR APPLICATION NUMBER: 08/862,178 OR FILING DATE: May 23, 1996 OR APPLICATION NUMBER: 09/081,589 OR FILING DATE: June 24, 1997                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R FILING DATE: July 31, 1996
R APPLICATION NUMBER: 08/903,556
R FILING DATE: July 31, 1997
R FILING DATE: AUGUST 22, 1996
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R APPLICATION NUMBER: 08/937,142
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APPLICATION UNBER: 60/026,598
FILING DATE: September 24, 1996
APPLICATION NUMBER: 08/960,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: June 25, 1996
APPLICATION NUMBER: 08/903,802
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APPLICATION NUMBER: 60/023,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: September 27, 1991
APPLICATION NUMBER: 60/005,526
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APPLICATION NUMBER: 08/905,881
FILING DATE: August 1, 1997
PALICATION NUMBER: 60/025,204
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APPLICATION NUMBER: 60/025,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: November 18, 1997 PRIOR APPLICATION NUMBER: 08/395,244 PRIOR APPLICATION NUMBER: 08/722,922 PRIOR APPLICATION NUMBER: 08/722,922
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APPLICATION NUMBER: 08/903,471
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APPLICATION NUMBER: 60/030,144
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100.0%; Pred. No. 0.35;
.ive 0; Mismatches 0; Indels
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; OTHER INFORMATION: Incyte ID No: hu00855921
US-09-540-2108-23868
PRIOR FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 08/903,471
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PRIOR FILING DATE: MARCH 12, 1998
PRIOR FILING DATE: MARCH 12, 1998
PRIOR FILING DATE: MARCH 12, 1997
PRIOR FILING DATE: MARCH 14, 1997
PRIOR FILING DATE: JUL 11, 1997
PRIOR FILING DA
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Best Local Similarity
Matches 21; Conserv
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OR APPLICATION NUMBER: 08/826,847
OR FILING DATE: April 10, 1997
OR APPLICATION NUMBER: 60/015,533
OR FILING DATE: April 10, 1996
OR APPLICATION NUMBER: 08/755,524
OR FILING DATE: November: 22, 1996

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Gaps

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1134 ccaaaacctggcatttgccta 1154 CCAAAACCTGGCATTTGCCTA 16

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Conservative

us-09-882-694a-10.rnpn

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Sequence 9536, Application US/09540210B GENERAL INFORMATION:
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APPLICATION NUMBER: 08/826,847
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                     929 GAGCGCACTCACACCACTGC 910
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100.0%; Pred. No. 1.1;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13179, Application US/10105299
GENERAL INFORMATION:
FAPLICANT: ROSen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105, 299
CURRENT FILEN DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
FILO APPLICATION TEMOVED - See File Wrapper or Palm
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 21; DB 5;
100.0%; Pred. No. 0.35;
iive 0; Mismatches (
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US-09-540-2108-31943
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PRIOR FILING DATE: FEDTUARY 10, 1998
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PRIOR FILING DATE: FEDTUARY 13, 1973
PRIOR FILING DATE: FEDTUARY 13, 1973
PRIOR FILING DATE: MATCH 4, 1998
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PRIOR FILING DATE: MATCH 12, 1998
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PRIOR FILING DATE: MAY 8, 1998
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PRIOR FILING DATE: MAY 9, 1997
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PRIOR FILING DATE: MAY 9, 1997
PRIOR FILING DATE: JULY 1, 1997
PRIOR PRIOR PRIOR PRIOR 1998
FILING DATE: November 22, 1995
APPLICATION NUMBER: 09/021,031
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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FEATURE:
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; ORGANISM: Homo sapiens
US-10-105-299-13179
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US-10-105-299-13179/c
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APPLICATT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029G30APID2
CURRENT APPLICATION NUMBER: 08/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: 60/089,507
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                    LOCATION: (78)
COTHER INFORMATION: n equals a, L, g, or c
NAME/KEY: SITE
LOCATION: (948)
OTHER INFORMATION: n equals a, L, g, or c
US-10-115-123-109
PRIOR FILING DATE: 1990-00. 20
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1990-06-22
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 109
LENGTH: 1487
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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; ORGANISM: Homo sapiens
US-10-105-299-11641
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US-10-115-123-109/C

Sequence 109, Application US/10115123
Sequence 109, Application US/10115123
GENERAL INPORMATION:
APPLICANT: Ruben et al.
TILE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029630APLD2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
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; OTHER INFORMATION: Incyte ID No: hu00667909
US-09-540-210B-9536
PRIOR PELICATION NUMBER: 60/015,533
PRIOR FILING DATE: April 10, 1996
PRIOR FILING DATE: November 22, 1996
PRIOR FILING DATE: November 22, 1996
PRIOR PRICATION NUMBER: 60/007,495
PRIOR PELING DATE: November 22, 1996
PRIOR PELING DATE: November 22, 1996
PRIOR PELING DATE: PEDRUARY 10, 1998
PRIOR PELING DATE: FEBRUARY 13, 1997
PRIOR PELING DATE: PEBRUARY 13, 1997
PRIOR PELING DATE: MARCH 4, 1998
PRIOR PELING DATE: MARCH 4, 1998
PRIOR PELING DATE: MARCH 5, 1997
PRIOR PELING DATE: MARCH 1998
PRIOR FILING DATE: MARCH 1998
PRIOR PELING DATE: MARCH 1998
PRIOR FILING DATE: MARCH 1999
PRIOR FILING DATE: MARCH 1997
PRIOR PELING DATE: MARCH 10, 1997
PRIOR PELING DATE: MARCH 10, 1997
PRIOR FILING DATE: MAY 8, 1998
PRIOR FILING DATE: JULY 1, 1997
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Best Local Similarity 100.C
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SOFTWARE: PERL Program
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT PILITATION UNBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
PILOT APPLICATION removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 253
LENGTH: 2495
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6763
LENGTH: 3291
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; GENERAL INFORMATION:
APPLICANT: ROSen, et. al
TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
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100.0%; Pred. No.
tive 0; Mismatch
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; OTHER INFORMATION: n equals a,t,g, or
US-10-105-299-253
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2-10-10-299-6763
; Sequence 6763, Application US/10105299
; GENERAL INFORMATION:
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100.0%; Pre
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                                    668 aggccaggatcaccagga 685
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Best Local Similarity 100.4
Matches 18; Conservative
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Best Local Similarity 100.0
Matches 18; Conservative
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US-10-105-299-253
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE REFERENCE: P2029G30APID2
CURRENT PILING DATE: 2002-04-04
RICHERIA APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 1999-06-15
REIOR APPLICATION NUMBER: ECT/US99/13418
PRIOR PLICATION NUMBER: ECT/US99/13418
PRIOR PLICATION NUMBER: 60/089,509
REIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PLICATION NUMBER: 60/089,509
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR PRIOR PILING DATE: 1998-06-16
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 532
SOCTUMARE: PATENTIN VET: 2.0
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100.0%; Pred. No. 14;
tive 0; Mismatches
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; OTHER INFORMATION: n equals a, L, g, or c
US-10-115-123-26
                     PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-16
PRIOR PELING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22
SOFTWARE: PALENTIN VGT: 2.0
SEQ ID NO 110
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; OTHER INFORMATION: n equals a,t,g, or
US-10-115-123-110
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LOCATION: (1130)
OTHER INFORMATION: n equals a,t,g, or
PRIOR FILING DATE: 1998-06-16
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Best Local Similarity 100.(
Matches 18; Conservative
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Best Local Similarity 100.0
Matches 18; Conservative
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LOCATION: (78)
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FILING DATE: June 24, 1997
APPLICATION NUMBER: 60/021,275
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 TYPE: DNA
ORGANISM: Homo saplens
US-10-103-313-604
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LENGTH: 32121
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Mismatches 0; Indels
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APPLICANT: ROSEN. et. al.
TITLE OF INVENTION: et. al.
TITLE OF INVENTION: Human Secreted Proteins; FILE REFERENCE: PS950
CURRENT FILING DATE: 2002-03-26; NUMBER OF SEQ ID NOS: 15197; PTIOR Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6769
ILENGTH: 3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSEN, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6768
LENGTH: 3291
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
CUMBER OF SEQ ID NOS: 15197
Prior Application removed - See File Wrapper or Palm SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 6764
LENGTH: 3291
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Mismatches
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Pred. No.
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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Matches 18; Conservative 0;
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; ORGANISM: Homo sapiens
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APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Angelo M.
APPLICANT: Studer, Susan G.
APPLICANT: Studer, Susan G.
APPLICANT: Studer, Susan G.
APPLICANT: Studer, Studen G.
APPLICANT: Mullahy, Sara J.
APPLICANTION: POLYNUCLECTIDES OF URINARY TRACT TISSUE FILE REFERENCE: PD-1037 CIP 00/8702-099
FILE REFERENCE: PD-1037 CIP 00/972-099
PRIOR APPLICATION NUMBER: 08/972-099
PRIOR APPLICATION NUMBER: 08/995-044
PRIOR FILING DATE: September 27, 1995
PRIOR PILING DATE: September 27, 1995
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR APPLICATION NUMBER: 08/824,029
PRIOR PILING DATE: March 25, 1997
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PRIOR PILING DATE: July 31, 1997
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                                                                                                   APPLICATE: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBUCE: PJZ07101

CURRENT APPLICATION NUMBER: US/10/103,313

CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 653

Prior Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0
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Mismatches 0
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APPLICATION NUMBER: 60/018,217
FILING DATE: May 23, 1996
APPLICATION NUMBER: 08/881,589
FILING DATE: June 24, 1997
US-10-103-313-604/c; Sequence 604, Application US/10103313; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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PRIOR FILING DATE: July 31, 1997
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PRIOR PAPLICATION UNBERS: 06/023, 308
PRIOR PAPLICATION UNBERS: 06/025, 204
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Query Match 0.4%; Score 17; DB 5; Length 242; Best Local Similarity 100.0%; Pred. No. 48; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	, Appl	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	5, Ap	5, Ap	230,	۷.	۹.		σ,	6	ď	ò	9, Ap
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8562 Sequence 18562, A 61 Sequence 161, App 83 Sequence 283, App 840 Sequence 283, App 850 Sequence 1, App11 850 Sequence 1, App11 850 Sequence 664, App 64 Sequence 664, App 64 Sequence 664, App 65 Sequence 664, App 65 Sequence 67, App 7 Sequence 20, App1 850 Sequence 20, App1	1.0. Application US/09351224  1. M. Application US/09351224  1. M. Application US/09351224  1. M. Application US/09351224  1. M. M. Davico.  1. M. M. Davico.  1. M.
US-09-404-520-188 US-60-132-861-166 US-60-138-103-944 US-60-138-103-944 US-09-404-520-288 PCT-US98-273-00-3 US-60-380-273-108-603 US-60-183-708-603 US-60-183-791-664 US-09-534-859-20 US-09-534-859-20 US-09-529-412-223	UULT 1  09-351-224-10  109-351-224-10  109-351-224-10  APPLICANT: DAVIGK, JON  FILE REFERENCE: 5718-111  CURRENT APPLICATION UNBER: US/09/351,224  CURRENT FILING DATE: 1999-07-12  CURRENT FILING DATE: 1999-07-12  SOFTWARE: Patentin Ver. 2.0  LENGTH: 3792  TYPE: DNA  ORGANISM: Exophiala spinifera  FEATURE: OTHER INFORMATION: p-glycoprotein, coding secons arches and methods  OFFICE STORMATION: p-glycoprotein, coding secons arches and methods  NUMBER OF SEQ ID NOS: 11  SOFTWARE: Patentin Ver. 2.0  LENGTH: 3792  TYPE: DNA  ORGANISM: Exophiala spinifera  FEATURE: OTHER INFORMATION: p-glycoprotein, coding secons arches and proposed approaches arches a
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1.0CATION: (0)...(0)
1. OTHER INFORMATION: p-glycoprotein, fully
02-09-351-224E-10
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ORGANISM: Exophiala spinifera
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Best Local S:
Matches 3792
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δλ	3361	ccgaattatcagaagagctttgtcaaggac
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δy	3601	coctogatgaggcatccacgagccgaacgacaatagcagtggcgcaco
QQ	3601	ctcgatgaggcatccacgagccgaacgacaatagcagtggcgcaccgacttccac
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Pred. No. 0;
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                                                                               US/09/351,823
                                                                  and
                                                                                                                                           ; OTHER INFORMATION: p-glycoprotein, US-09-351-823-10
                                                       APPLICANT: DUVICK, JOA
TITLE OF INVENTION: Compositions an
FLIE REFERENCE: 5718-56
CURRENT APPLICATION NUMBER: US/09/3
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VEY. 2.0
                                           Sequence 10, Application US/09351823 GENERAL INFORMATION:
                                                                                                                                                                                       ;
                                                                                                                                                                           Query Match

Best Local Similarity 100.0%;
Matches 3792; Conservative 0;
                                                                                                                         TYPE: DNA
ORGANISM: Exophiala spinifera
RESULT 3
US-09-351-823-10
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APPLICANT: Duvick, Jon TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification FILE REFERENCE: 35718/204100 (5718-111A )
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CURRENT APPLICATION NUMBER: US/09/677,488
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 10
                                                                                OTHER INFORMATION: p-glycoprotein,
                                                                                                            100.0%;
100.0%;
                                                                  spinifera
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                                                           TYPE: DNA
ORGANISM: Exophiala
FEATURE:
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Oy 1921 cgagaagctgctggtgaacgaccttgagcgactcacaccactccaa 1980		atgc 228      atgc 228 actg 234 	Oy 2341 gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa 2400	ctggg 25         ctggg 25 attcg 25 	Oy 2581 tctagagacgaagctagaagccggaaactcggcaaactttgcagaaagtgctgggcttgc 2640	Oy 2701 ccaacagtactcggacatgttgagcaaggtcttgctaagatcatccaaagcttttggttt 2760 	Oy 2761 ggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgcctggga 2820

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FRStSEQ for Windows Version
; SOFTWARE: PRSTSEQ for Windows Version
; LENGTH: 3792
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: p-glycoprotein, fuus.09-677-488A-10
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RESULT 7
US-09-677-682A-10
Sequence 10, Application US/09677682A
Sequence 10, Application US/09677682A
Sequence 10, Application US/09677682A
Sequence 10, Application US/09677682A
Sequence 10, Application Sequence 10, APPLICANT: Duvick, Jon
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Carasta, Oswald R.
TITLE OF INVENTION: Detoxification
TITLE OF INVENTION: Detoxification
TITLE OF INVENTION: Detoxification
STILE REPRENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,682A
CURRENT PILING DATE: 2000-10-02
PRIOR FILING DATE: 1999-07-12
SOFTWARE FEASTSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: p-glycoprotein, fully spliced cDNA
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LENGTH: 3792
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    LOCATION: (0)...(0)
    COTHER INFORMATION: p-glycoprotein, fully spliced
    WS-09-882-694-10

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GENERAL INFORMATION:
APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Me;
TITLE OF INVENTION: Detoxification
FILE REFERENCE: 35/18/208255
CURRENT APPLICATION NUMBER: US/09/882, 6;
CURRENT FILING DATE: 2001-06-12
PRIOR FILING DATE: 1999-07-12
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
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US-09-882-694-10
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LENGTH: 379
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Query Match Best Local Similarity

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APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Metl)
FILE REFERENCE: 5718-111
CURRENT APPLICATION NUMBER: US/09/882,69,
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 1999-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                    RESULT 10
8.09-882-94A-10
Sequence 10, Application US/09882694A
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows
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APPLICANT: Maddox, Joyce
APPLICANT: Gilliam, Jacob
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Best Local Similarity 100.
Matches 3792; Conservative
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; LOCATION: (0)...(0)

; OTHER INFORMATION: p-gl

US-09-882-694A-10
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Sequence 9, Application US/09351224E
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Sequence 9, Application US/09351224E
SECONDERAL INFORMATION:
APPLICANT: Buddox, Joyce
APPLICANT: Gilliam, Jacob
APPLICANT: Crasta, Otto
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Decoxification
FILE REFERENCE: 5718-111
CURRENT APPLICATION UNMBER: US/09/351,224E
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFWWARE: FASTEED for MARCH
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OTHER INFORMATION: p-glycoprotein, 09-351-224E-9
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GENERAL INFORMATION:
APPLICANT: DUVICK, JON
TITLE OF INVENTION: Compositions and Methods for Funmonisin Detoxification
FILE REFERENCE: 5718-56
CURRENT PELLING NUMBER: US/09/351,823
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Duvick, Jon
TITLE OF INVENTION: Compositions and Meth
FILE REFERENCE: 35718/204100 (5718-111A)
CURRENT APPLICATION NUMBER: US/09/677,488
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
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ilarity 99.9%;
Conservative
                                                    PatentIn Ver. 2.0
                                                                             ORGANISM: Exophiala
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                                                                 LENGTH: 3999
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Best Local Simi
Matches 830;
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                                                                        TYPE: DNA
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SEQ ID NO 9
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                                                  Score 780; DB Pred. No. 0; 0; Mismatches
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                           p-glycoprotein,
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LENGTH: 3999
TYPE: DNA
ORGANISM: Exophiala spinifera
                                                  atch 20.6%;
cal Similarity 99.9%;
830; Conservative
                   FEATURE:

COTHER INFORMATION:

US-09-351-823-9
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US-09-677-488-9
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                              APPLICANT: Duvick, Jon
APPLICANT: Gliliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
TITLE OF INVENTION: Detoxification
FILE REFERENCE: 35718/204100
FILE REFERENCE: 3000-10-02
FRIOR APPLICATION NUMBER: 09/351,224
FRIOR APPLICATION NUMBER: 09/351,224
FRIOR FILENG DATE: 1005: 11
SOFTWARE: FastSEO for Windows Version 4.0
                 gatgtctttttgcagcaagcacaccaagaagggaagaagaaatcgccaaat
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Pred. No. 0;
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LOCATION: (0)...(0)
CTHER INFORMATION: p-glycoprotein,
US-09-677-488A-9
                                                                                                             Sequence 9, Application US/09677488A GENERAL INFORMATION:
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Best Local Similarity 99.9
Matches 830; Conservative
                                                                                   RESULT 15
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	Description	Exophiala spinifer	Exophiala spinifer	cDNA encoding mult	Human ovarian carc	Human breast cance	Human breast cance	Staphylococcus aur	Human immune/haema	Human immune/haema
SUMMARIES	ΩI	AAD02695	AAD02694	AAX85823	AAA69756	AAL16237	AAL25080	AAV74548	AAK75234	AAK59415
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	Prote Human Human Human B. ep B. ep Cook B. ep Genom Human B. ep		ALIGNMENTS  ein coding sequence.  transport enzyme; flavin monooxygenase; e; p-glycoprotein; fumonisin esterase; al feed; human feed; silage; imal; microbial spray; ds.  iers  pinifera p-glycoprotein"
AH67255 AAF71942 AAK75237 AAC34294 AAH53092 AAS56128 AAK82911 AAH55046	NAX52267 NAC5859C NAF72425 NAF72425 NAF15614 NAF1575 NAF1372 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373 NAF1373	AAK6562 ABL13742 ABL13742 AAC8138 AAC84070 AAC39682 AAC39682 AAC64561 AAF66406 AAF66406 AAF66406 AAF91072 AAF91072 AAC528856 AAC528856 AAC528856	try) glycoprotein codin glycopro
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WPI; 2001-147345/15. P-PSDB; AAY72637. Maddox JP, Duvick 

The patent discloses novel polynucleotides encoding Exophiala spinifera fumonish degradative or transport enzymes such as flavin monooxygenses, aldehyde dehydrogenses, permease and p-glycoprotein. A fumonish esterase enzyme with at least one fumonish degradative enzyme is useful for enzyme with at least one fumonish degradative enzyme is useful for detoxifying fumonish or a structurally related mycotoxin present in harvested grain, on application to a plant or to harvested grain of during processing, or to processed grain that is to be used as animal corruption are useful as probes and primers. They can be introduced into microorganisms that multiply on plants to deliver enzymes to introduced via a vector into a microbial host and the transformed host is supplied to the environment, plants or animals for reducing the pathogenicity of a fungus producing fumonish. The genes of the processed and used as a microbial spray. The nucleotide sequences is processed and used as a microbial spray. The nucleotide sequences or or numerabolisms to metabolish spray. The nucleotide sequences or or metabolish mad reasist its toxic effects.

The present DNA sequence is the p-glycoprotein coding sequence Novel polynucleotides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal consumption Claim 1b; Page 75-77; 90pp; English.

T; 2 other; G; 940 C; 928 Sequence 3792 BP; 939 A; 983

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functional degradative or transport enzymes such as flavin monoorgenase, aldehyde dehydrogenase, permease and p-glycoprotein. A funchisin esterase enzyme with at least one funconisin degradative enzyme is useful for detoxifying funchisin or a structurally related mycocoxin present in harvested grain, on application to a plant or to harvested grain or to processed grain that is to be used as animal or human feed, or as a silage. Nucleotide fragments of the present or human feed, or as a silage. Nucleotide fragments of the present or human feed, or as a silage. Nucleotide fragments of the present or hororizonganisms that multiply on plants to deliver nezymes to potential target crops. The genes encoding the degrading enzymes are introduced via a vector into a microbial host and the transformed host or supplied to the environment, plants or animals for reducing the pathogenicity of a fungus producing fumonisin. The genes of the resulting bacterial is processed and used as a microbial spray. The nucleotide sequences can be used alone or in combination to engineer microbes or other organisms to metabolise fumonisin and resist its toxic effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patent discloses novel polynucleotides encoding Exophiala spinifera
                                                                                                                                                                                                 Fumonisin; degradative enzyme; transport enzyme; flavin monooxygenase; aldehyde dehydrogenase; permease; p-glycoprotein; fumonisin esterase; detoxification; mycotoxin; animal feed; human feed; silage; transgenic plant; transgenic animal; microbial spray; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynuclectides encoding Exophiala degradative or transport enzyme which is useful for detoxifying fumonisin or structurally related mycotoxin during processing of grain for human or animal food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Folkerts O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-glycoprotein, a fumonisin degradative enzyme
                                                                                                                                                                            Exophiala spinifera p-glycoprotein genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1b; Page 74-75; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilliam J,
                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC (CURA-) CURAGEN CORP.
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                    cetececeagaaaaggaaacegaaggeagtattteagaetatetaegaatetteagatat
                                                                                                                                                                                                                                                                                                                                                 Multiple drug resistance; atrD; fungal disease; antifungal; ss.
                                                                                                                                                                                                                                                                     cDNA encoding multiple drug resistance gene atrD
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Frudakis TN;

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immunogenic portion of an ovarian carcinoma protein (or its variants).

Ovarian carcinoma proteins, and polynuclectides encoding them, have cytostatic activity and can be used in gene therapy and vaccines.

Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in
                                                                        Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer.
                                                                                                                                                        The present invention describes an isolated polypeptide comprising an
                    Algate PA,
                                                                                                                             Claim 1; Fig 1; 299pp; English.
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                  Mitcham JL,
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; identification; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                The present sequence encodes a multiple drug resistance protein, designated atrD, which is isolated from Aspergillus nidulans. The atrD polynucleotide is used to produce nucleic acid molecules which are useful in diagnostic assays for the detection of atrD polynucleotides. The atrD polypeptide may be used to identify agents which inhibit multiple drug resistance. These agents may be useful for the treatment of fungal diseases. New antifungal compounds also be identified using the gene disruption or gene replacement
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100.0%; Pred. No. 5.6;
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                                                                                                                                                                                                            Peery RB,
                                                                                                                                                                                                                                                                                                       Claim 2; Page 21-27; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aspergillus nidulans
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(UYWA-) UNIV WAGENINGEN AGRIC
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99US-0338933.
99US-0404879.
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                                                                                                                                                                                                         De Waard MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                  WPI; 1999-418917/35.
P-PSDB; AAY02630.
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les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ovarian
                                                     WO9932608-A1
                                                                                                                                       23-DEC-1997;
                                                                                                            22-DEC-1998;
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24-SEP-1999;
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                                                         Length 359;
                                                                               0; Indels
                      Sequence 359 BP; 125 A; 69 C; 82 G; 82 T; 1 other;
                                                                                                                                                                                                                                                       Human breast cancer expressed polynucleotide 8694.
                                                                                                                                                                                                                                                                             Human; breast cancer; cell marker; cytostatic; ss.
                                                        21;
the exemplification of the present invention.
                                                       0.5%; Score 20; DB;
100.0%; Pred. No. 18;
tve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1573; 3695pp; English.
                                                                                                                                                                                      BP.
                                                                                                      2209 ttttatattctgatgttctt 2228
                                                                                                                  287 TTTTATATTCTGATGTTCTT 268
                                                                    100.08;
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2000US-0189167,
2000US-0192099,
2000US-0193480,
2000US-0205230,
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          expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells
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                                                                                                                            Sequence 490 BP; 154 A; 107 C; 106 G; 121 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cancer expressed polynucleotide 17537
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                                                                                                                                                                           Score 20;
Pred. No.
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100.08; Pre-
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2000US-0189167.
2000US-0192099.
2000US-0193480.
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2000US-0211315
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                                                                                                                                                                                                           Conservative
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Best Local Similarity
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15-MAY-2000;
09-JUN-2000;
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Length 702;

DB 22; 18;

Score 20; Pred. No.

0.5%; 8

Query Match Best Local Similarity

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/*tag= a // note= these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence. 2881..2940 /*tag= b // note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence. 4681..4740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access the S. aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag* c // these bases represent a line of missing text in /note* the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence*
                                                                                                                                                                                                                 Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food polsoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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in the production of
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                                                                                                                                                                                          Staphylococcus aureus contig SEQ ID #237.
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1081..1140
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(first entry)
                                                                                                       standard; DNA;
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        18-AUG-2000;
22-AUG-2000;
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14-SEP-2000;
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be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellultis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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100.0%; Pred. No. 18;
tive 0; Mismatches 0; Indels
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2000US-0180628.
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2000US-0215135.
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2000US-0217496.
2000US-0220963.
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2000US-0209467
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2000US-0198123
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                            computer readable medium.
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17-MAR-2000;
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AAK59415 standard; cDNA; 247 BP

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AAK59415 RESULT

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(HUMA-) HUMAN GENOME SCI INC
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06-NOV-2001
AAK59415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis –
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100.0%; Pred. No. 60;
.ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 19; Conservative
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                            Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4475
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22.5EP-2000;
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ANK54931 to AAK64702 encode the human immune/haematopoletic antigen (I) and action sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polyvucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 concers and cancer human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK54950 and AAM82169 corporation.
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4475; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                 Ruben SM;
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2000US-0250160.
2000US-0250391.
2000US-0251030.
2000US-0256719.
2000US-0251479.
2000US-0251866.
2000US-0251868.
2000US-0251869.
2000US-0251869.
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   2000US-0249299
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P-PSDB; AAM86634.
17-NOV-2000; 2
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01-DEC-2000; 2
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05-DEC-2000; 2
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Corynebacterium glutamicum.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Ikeda M, Ozaki A;
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                                                                                                 18-DEC-2000; 2000EP-012768B.
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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Senoh A, Ik
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Tateishi N,
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Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
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20000S-02346178.
20000S-0241809.
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                                                                                    AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches
                               Claim 3; Page 723-724; 1737pp; English
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24-FEB-2000; 2000US-0186628.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                  AAC34294;
                                                                                                    ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vacchine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the ucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 30049; 3071pp + Sequence Listing; English.
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28 - JUL - 1999;
28 - JUL - 1999;
28 - JUL - 1999;
02 - AUG - 1999;
04 - AUG - 1999;
04 - AUG - 1999;
05 - AUG - 1999;
06 - AUG - 1999;
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13-AUG-1999;
16-AUG-1999;
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20-JUL-1999;
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Gaps

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us-09-882-694a-10.rng

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Salmonella typhi DNA for cellular proliferation protein #161.
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  AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the secondariant them white are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them white as to produce hosts cells which express the polypeptides. The polypeptides and to raise antibodies against the bacteria. The polypeptides and to raise antibodies against the bacteria. The polypeptides and to raise antibodies against the bacteria. The polypeptides and to raise antibodies against the bacteria. The polypeptides and so used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55091 represent specifically claimed S. epidermidis genomic DNA polypucleotide sequences from the present invention. AAH55091 to AH55099 represent conservation of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                  S. epidermidis open reading frame nucleotide sequence SEQ ID NO:1577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 19; DB 22; Length 1224;
100.0%; Pred. No. 59;
1ve 0; Mismatches 0; Indels
                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1224 BP; 384 A; 199 C; 219 G; 422 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 443; 2188pp; English.
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100.0%; Pre-
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                                                                                                                                                                                                                09-NOV-2000; 2000WO-US30782
                                                                                                                                  Staphylococcus epidermidis
                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                     GLAX ) GLAXO GROUP LTD
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                                                                                                                                                             WO200134809-A2
                                                                                                                                                                                                                                          09-NOV-1999;
                                      03-SEP-2001
                                                                                                                                                                                                                                                                                               Kimmerly WJ;
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                                                                                                                                                                                       17-MAY-2001
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             AAH53092;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are carberichia coli, Staphylococcus aureus, Salmonella Eyphi, Klebsiella pneumoniae, Pseudomonsa aeruginosa and Enterococcus feecalis. The invention is also useful for the Identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick JD,
Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Seq ID No 9765; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL, Zyskind JW,
Xu HH;
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Job time: 13897 sec
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC
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P-PSDB; AAU38269.
                                                                                                       Salmonella typhi.
                                                                                                                                                                          WO200170955-A2
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26-MAY-2000;
23-OCT-2000;
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Yamamoto RT,
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22-DEC-2000;
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AX076851 Sequence
AX076850 Sequence
AX076850 Sequence
AE005604 Escherich
AE000450 Escherich
X01631 E. coli ori
L10328 E. coli; th
AP002566 Escherich
AF126398 Mus muscu
EC002275 Mus muscu
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AR149777 Sequence
AR173826 Emericell
AF071411 Aspergill
AF123502 Mus muscu
AE006358 Lactococc
L78821 Mycobacteri
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AL161785 Human DNA
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AL078459 Human DNA
AC066932 Genomic s
AC049651 Human DNA
AC049651 Human DNA
AL39015 Human DNA
AL39015 Human DNA
AL39015 Human DNA
AL39013 Human DNA
AL59113 Homo sapi
AC106083 Rattus no
BC017424 Homo sapi
AC1607 T. vaginalis
X76160 T. vaginalis
L41933 Mus musculu
AC062117 Halobacte
AC108249 Rattus no
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Exophiala spinifera

Exophiala spinifera

Eudaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;

Chaetothyriales; Herpotrichiellaceae; mitosporic

Herpotrichiellaceae: Exophiala.

1 (bases I to 3792)

1 (bases I to 3792)

1 (chaetothyriales; Maddox,J., Gilliam,J., Folkerts,O. and Crasta,O.R.

Compositions and methods for fumonisin detoxification

Patent: WO 0105980-A 10 25-JAN-2001;

Ploneer Hi-Bred International Inc. (US); Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapi
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Squence 10 from Patent W00105980.
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AX076851.1 GI:13121523
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AX076850
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AE005604
AE000450
ECUNC
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AR149777
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AR13502
AR123502
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AR1890113
AR1800188
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AC108249
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VERSION
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AUTHORS
TITLE
JOURNAL
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                     1797656 segs, 10463268293 residues
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                                                                      nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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c dg	121 gccgacaaatacgactggactctcaatgtcatcgcgctcatctgcgccatcgggtccggg	Qy
Oy 1	181 gcttccttcttcttgatgtcgatcatcttcggtagcttcaccaacaagttcaacaatac 240 	oy Oy
oy coy	241 aattogggcgacgggagtcctgaagcgttcaaggccgatgtggatcatttcgtcctgtgg 300 	oy Dp
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رة د. د.	361 atttcagctatacgaaccactcgaactcttcgacgagtgttccttgaatgcaccttgcgg 420 	oy Ob
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qq	1021	AACGCCGCATCTTCGGCTCCGAATTATTCAGTATCATTGACAAACCCACGCAGCTCGAC 108
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Qy	1681	gtccaggaggcttgaaccgagtgtccaaagaccgcactactttggtcattgccacaaa 1740
qq	1681	rccaggaggccttgaaccgagtgtccaaagaccgcactactttggtcattgggcacacaaa 174
ογ	4	0
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ογ	1801	caaggcacacaccacgaattgatcgaattcggctgtcattacgccgcactggtgcgtgc
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δλ	1861	Ċυ.
aa	1861	SGACCTCGGGGCTGACGAACAACAACATGAGAAGACCCTGCACGAAAAGGCAGCA 192
Οy	1921	gccacatctcaa 198
qq	1921	gadaagcigciggigaacgaccggcaciigagcgcacicacaccacigccacaictea 198
ογ	1981	Ecgetectaaaa 204
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δλ	2041	10
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2101 ataacggttctgatatgcgcggccacatttccaggacaagccttttgttttcgagatt 	2161 CTCACTGTTTCGAGTGGTGATGGGGCAGGGAGGGCAGCATTTTTTTT	/ 2281 aacgttatttcacaagttgtcacccatcgctatcaagccgcaatgttccaacgagtactg	/ 2341 gatcaagacatcgaactcctcgacatcccggagcaaatttctggtgctctcacatcgcaa	/ 2401 ctgtcagctctacccacgcagttgcaagattgtatatcagcaaatttctcatttatatc	/ 2461 gttgtcggtcaacatcgtctcgagcagtgcttaccactagcctatggatgg	7 2521 cctggtggttggtgtttggtgcacttccaccctgcttttggctggc	/ 2581 tctagagacgaagctagaagccggaaactcggcaaactttgcagaaagtgctgggcttgc 	/ 2641 aaggaagcagttaccgcgatccggaccgtctcatctttgactctcgaaggccatgttct	7 2701 ccaacaqtactcggacatgttgagcaaggtcttgctaagatcatccaaagcttttggttt	/ 2761 ggacgatgttttggttttcacttgtcacagtcgatggagtttttggctattgccctggga 	2821 ttttgtattgcagtcgataattggcttcaggtgagtacgacacaactcaattttatatca 	2881 tettogtggggttttgtttgccggtccaagcagcagccagtatttggttactccacg	/ 2941 agttttaccaaggctcggtcggtcggaactatatcctctggctgcggacattgaagccg	/ 3001 accatccgcgaaacggaggagaacaagaaaaaggcccagtgggtgg	3061 ctcgaggacattgaattcagtatcgtcaacgtgattcggctcgagttctccgcggggtt	/ 3121 tccatgacaatcgagccaggacaattgtagcttatgtgggcgcttctggctgtggcaggca
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Qy 33	01	caacaggaacccacactttaccaaggctccgttcgcgaaatgtgacgttggcctcgaa 3360 
Qy 33	61 61	gccgaattatcagaagactttgtcaagacgccttcccgcaaggccaatgctttggatt 3420 
Qy 34 Db 34	21	ttgtcatcttttaccagaaggctttgaacgccttgcggctcaacgaggatgcagttc 3480 
Qy 34 Db 34	81	tccggcgggcaacgacagcggatcgccatcgcaagagcattgattcgaaatccaaagctg 3540 
Qy 35.	41	ttgetacttgacgaagcgacgtcagccccgacacgcaatcggaacgtctggttcaagct 3600 
Oy 36	01 g   01 G	ccetcgatgaggcatccacgagccgaacgacaatagcagtggcgcaccgactttccact 3660 
Oy 36	61	attoggaatgttgatgttattttgtgtttgccaacgggagaatcgccgaaacgggcact 3720 
Qy 37 Db 37	21	cacgoggaactacaacgactgagaggaagatattacgagatgtgtttggcacaatcttta 3780 
Oy 37 Db 37	81 81	gaccaagcatga 3792  -
RESULT 2 AX076650 LOCUS DEFINITION ACCESSION VERSION KENEGODIS	0 0 0 O O O O O O O O O O O O O O O O O	AX076850 3899 bp DNA linear PAT 22-FEB-2001 Sequence 9 from Patent W00105980. AX076850 AX076850 GI:13121522
SOURCE	6	Exophiala spinifera. Exophiala spinifera Eukaryota: Fungi; Ascomycota: Pezizomycotina: Chaetothyriomycetes; Chaetothyriales; Herpotrichiellaceae: mitosporic
REFERENCE AUTHORS TITLE JOURNAI	F-1 76 . 1	neigoticinitacese; 1 to 3999; baopinata.  1 (bases 1 to 3999; baopinata.  Duvick,J.P., Maddox,J., Gilliam,J., Folkerts,O. and Crasta,O.R.  Compositions and methods for fumonisin detoxification Patent: WO 0105980-A 9 25-JAN-2001;  Diometr: WO 1015980-A 9 25-JAN-2001;  Diometr: Wo 1015980-A 1 1 to 1 1 to 1 1 to 1 to 1 1 to 1 to
FEATURE	S TI	. U.
BASE CO	COUNT	/note="r-glycoprotein, with introns" 1007 a 1008 c 992 g 987 t 5 others
Query Best	Match Local	ch l Similarity 99.9%; Pred. No. 0;

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2 (bases 1 to 10104)

Perna, N. T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J. D.,
Perna, N. T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J. D.,
Postai, G., Hackett, J., Klink, S., Boutin, A., Show, Y., Miller, L.,
Fortbeck, E. J., Davis, N. W., Lin, A., Duutin, A., Show, Y., Miller, L.,
Apodaca, J., Anantharaman, T. S., Lin, J., Yen, G., Schwartz, D. C.,
Walch, R. A. and Blattner, F. R.
Walch, R. A. and Blattner, F. R.
Bubmitted (22-OCT-2000) Laboratory of Genetics, University of
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 10104)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A. and Blattner, F.R.
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Nature 409 (6819), 529-533 (2001)
       Structure of the human type IV collagen COL4A6 gene, which is mutated in Alport syndrome-associated lelomyomatosis Genomics 33 (3), 473-479 (1996)
                                                  2 (bases 1 to 128)
Zhang, X.
Direct Submission
Submitted (24-JAN-1996) Xu Zhang, MBB, Karolinska, Stockholm,
171-77, Sweden
                                                                                                                                                                                                                 contains multiple X-chromosomes
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genome, contig 3 of
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Escherichia coll 0157:H7 EDL933
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/db_xref="taxon:155864"
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Escherichia coli 0157:H7 EDL933
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Catarrhini; Hominidae;
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominid
1 (bases 1 to 128)
Zhang,X., Zhou,J., Reeders,S.T. and Tryggvason,K.
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YLSGMPEKGEFLLSWGQAADEKCKAAYHITHKPDDTSLVQMDAICR"
complement(6074. .6235)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="massallfitlasgiclicsisafardslfnprlleldhpadnid
IHQFnrsnTlpagTYKvDVMINGMLFERQEVKFAQDNPDAELHPCYVAIKNVLATYGI
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                                                                                  /note="Residues 12 to 844 of 844 are 40.82 pct identical to residues 18 to 842 of 842 from GenPept 118 : gi1829373[gb|AAA73968.1] (U18559) lpfC gene product [Salmonella typhimurium]"
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complement(6376..6759)
/gene="25224"
/func="usez"/function="butative factor; Cell exterior constituents:
Surface structures"
/function="putative factor; Cell exterior constituents: Surface structures"
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/product="putative major fimbrial subuit"
/protein_id="AAG58930.1"
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/db_xref="GI:12518579"
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/product="putative fimbrial usher"
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/db_xref="GI:12518578"
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complement(6863..7465)
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Surface structures"
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Surface structures

/note="Residues" to 354 of 356 are 25.75 pct identical to residues 14 to 355 of 356 from GenPept 118;
gill787131gblaAAC74027.11 (AE000196) homolog of Salmonella FimH protein [Escherichia coli]"
                                                                                                                                                                                                                                     /note="Residues 1 to 346 of 346 are 99.71 pct identical to residues 1 to 346 of 346 from Escherichia coli K-12 Strain MG1655: B3728"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative fimbrial protein"
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/protein_id="AAG58925.1"
/brotein_id="AAG58925.1"
/brotein_id="AAG58925.1"
/translation="kKKWHYIFOII.PHLGLPCGYAANDGTCATRGGTHTLSINFPLT
TVSAANNVPGNTLIDIANATSSENYSVLCNCDSKHSNGAYHEIYYTADPAPGMVYSTT
TVSAANNVPGNTLIDIANATSSENYSVLCNCDSKHSNGATTTDHTCGGNKTTAVGVSIK
GGADAKISTRIRKSINGTVVPITDIALLYANISSTTTRGEALAKVRISGSLTAPQSC
GINAGQVYIFFDFDIAPASEFSSTAGGAITSKITKTVVSIECTGMGYBRTQKVDASFTG
INRSSDDTMVATDNADVGIKIYNKSNAEVSVNNGKLPADMGNTIFGRKNGSVTFSAA
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SIDVDFQKINSAEFSSTAGSIIAERKIKTEVTVSCTGMEDVRSTEVVSASMIAANRSA
DATMIVTSNPDVGIKIFDKNDRPVNVDGGNLPADMGAISRLGKTDGSVTFYSAPASLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Residues 22 to 358 of 360 are 27.90 pct identical to residues 22 to 355 of 356 from GenPept 118 : g1|1787173|gb|AAC74027.1| (AE000196) homolog of Salmonella FimH protein [Escherichia coli]"
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/protein_id="A4G58926.1"
/db_xref="Gi=251857"
/translation="MKXILSGLILLCCPYGFAANGDGATHMSNLSFGPLTVAAANNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPCALGY
VEYAYAKONNLAYTKLISADGKPVLPTEENFANAAKGADWSKTFAQDLTNQKGEDAWP
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TNIKDSSGKPLY"
1220. .8162
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YYALNDYLSVGVTIFIINNQYAAIPFEHLSNQSTSPQHTCGAGNNGSTVNLDSGRSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKVMRTTVATVVAATLSMSAFSVFAEASLTGAGATFPAPVYAKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLAQEGLFQFPTVIG
GVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1220. ,8162
/note="O-island #154; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
complement(1326. .2408)
/gene="Z5220"
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/product="high-affinity phosphate-specific transport
system: perilasmic phosphate-binding protein"
/protein_id="AAGS8924 1"
/db_xref="G1:12518575"
                                                                                                                                                                        function="transport; Transport of small molecules:
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/gene="x5221"
complement(2436..3506)
/gene="x5221"
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/gene="25220"
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complement(3518. .6052)
/gene="25222"
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                                                                                          complement(74. .1114)
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/transl_table=11
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        /gene="psts"
/note="Z5219"
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                   /translation="MKPNMIVGALALTSVFWAGHLQAADGTVHFRGEIIDSTCEVTPE
TYDQVYDLGKVNRTAFSGYDDVAAPTAFSIDLTQCPETFKSAAIRFOGNEDAHGNGNL
AIGTPLDNSNDAAAGISPSDNSGDYTGAGAVSAAKGVAIRLYNRADNTQVKLYENSAS
TPISNGNASWKENARTIATETTIDPGTANADSQFTVEYIK"
COMPLEMENT(7777. .7866)
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Escherichia coli K12 MG1655 section 340 of 400 of the complete
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Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V., Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y.
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This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using Genemark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Allanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Emall: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Escherichia.
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                                                                                                                                                                                                                 /function="orf; Unknown function"
/note="No significant matches"
                                                                                                                                                                                                                                                                                                          /protein_id="AAG58931.1"
/db_xref="GI:12518582"
                                                                                                                                         /gene="25226"
complement(7777. .7866)
/db_xref="GI:12518581"
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AE000450.1 GI:1790166
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Blattner, F.R.
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Escherichia coli K12
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Direct Submission
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Matches 22; Conserv
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Locus

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have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site. (http://www.genetics.wisc.edu). *** The E. coli Kl2 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courresy of Monica Riley: added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein - or RNA-encoding) should allow them to be searched for in Entrez as gene names.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic evidence for the site"

// Abound_molety**PhoB predicted site"

// Complement(67. 84)

// Anote**central position to phoS promoter: -37*

// Abound_molety**PhoB documented site*

// Complement(67. 84)

// Anote**central position to predicted promoter: -37;

// Abound_molety**PhoB predicted site*

// Abound_molety**PhoB predicted site*

// Abound_molety**PhoB predicted site*

// Abound_molety**PhoB predicted site*

// Anote**central position to predicted promoter: -47;

// Anote**Central position to predicted promoter: -4
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/note="factor Sigma70; promoter phos; documented +1 at 3909196"
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/bound_moiety="PhoB documented site"
complement(66. .83)
/note="central position to predicted promoter: -36;
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complement(2238. .2265)
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/organisma-Escherichia coli K12"
/strain="K12"
/sub_atrain="MG1655"
/db_xref="taxon:83333"
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/db_xref="G1:1790167"
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/transl_table=11
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/note="b3729"
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MELIRNIAIEHSGYSVFAGVGERTREGNDFYHEMTDSNVIDKVSLVYGOMNEPPGNRL
RVALGGITMAEKFRDEGRDVLLFVDNIYRYTLAGTEVSALLGRMPSAVGYOPTLAEEM
GVLQERITSFRGSTTSVQAVYVPADDLTDESPATTFAHLDATVVLSRQIASLGIYPA
VDPLDSTSRQLDPLVVGGEHYDTARGVQSILQRYQELKDIIAILGMDELSEEBKLVVA
RARKIQFELSOPFFVAEVFTGSPGKYVSLKDTIRGFKGIMEGEYDHLPPQAFFWVGSI
EEAVEKAKL
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/translation="WEYPDPPDY1112"
/translation="WEYPDPPDY111GGGHAGTEAAMAAARWGQGTLLLTHNIDTLGQ
MSCNPAIGGIGGHLVKEVDALGGLHAKADDAGIQFRILMASKGPAVRATRAQADRY
LYRQAVRTALENQPHMAIFQQAVEDLIVENDRYVGAYTQMGLKFRAKAVVLTVGFFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECUNC 14526 bp DNA linear BCT 29-APR-1998 E. coli origin of replication oriC and genes gid, unc, EcoURF-1 and
  GEEERWAIHRAAPSYEELSNSQELLETGIKVIDLMCPFAKGGKVGLFGGAGVGKTVNM
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1 (bases 1 to 14526)
Walker,J.E., Gay,N.J., Saraste,M. and Eberle,A.N.
DNA sequence around the Escherichia coli unc operon. Completion of the sequence of a 17 kilobase segment containing asnA, oriC, unc,
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Messer,W., Hartmann-Kuehlein,H., Langer,U., Mahlow,E., Roth,A.,
Schaper,S., Urmoneit,B. and Woelker,B.
The complex for replication initiation of escherichia coli
Chromosoma 102, 1-6 (1992)
                                                                                                                                                                                                                                                              Gaps
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X01631.1 GI:43256
inverted repeat; origin of replication; transposable element.
Escherichia coli.
Escherichia coli.
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407. .2293
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/note-"pot. promoter -35 region"
367. .372
/note-"pot. promoter -10 region"
395. .398
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/db_xref="SWISS-PROT:P03817"
/translation="GSWVNLLK"
                                                                                                                                                                                                  0.6%; >cc.
100.0%; Pred. No. c.
0; Mismatches
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/protein_id="CAA25773.1"
/db_xref="G1:43257"
                                                                                                                                                               complement(4519. .4548)
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1. .14526
/organism="Escherichia
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                                                                                                                                                                                                                                                              Conservative
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glms.
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KEYWORDS
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/db_xref="G1:1790168"
/tb_xref="G1:1790168"
/translat.on-"MLNNAWVILAAGKGTRNYSDLPKVLHTLAGKAMVQHVIDDAN
ELGAAHVHLVYGHGGDLLKOALKDDNLNWVLQAEQLGTGHAMQQAAFFADDEDILML
YGDVPLISVETLQRLRDAKPQGGIGLLTVKLDDPTGYGRITTENGKVTGIVEHKDATD
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/translation="NAMTYHDVVSARQQMFSGLVEKIQVTGSEGELGIYPGHAPLLT
/translativKQHGHEFTYLSGGILEVQPGNVTVLADTAIRGQDLDEARAMEAKRKA
EEHISSSHGPVDYAAASAELAKAIAQLRVIELTKKAM"
complement(4446. .5828)
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VNIIEGNVTICHRVK GTGCVTKNSVTGDDCETSPYTVVEDARLAAGARLAAGTIGFPRILRP
GVBILGGAHVGHVENKRARLGKGSRAGHTPYLGDAETGDNNNIGAGTITCRYDGANK
FKTIIGDDVFVGSDTQLVAPVTVGKGATIAAGTTVTRNVGENALAISRVPQTQKEGWR
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OOLGGGIVRTIAMGSSDGLRRGLDVKDLEHPIEVPVGKATLGRIMNVLGEPVDMKGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQROIQEINTGILIANGADMKRWLAKLTNNNAQGEYYITDIIALAYQEGREIVAVHPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Joue="central position to predicted promoter: -224.5"
/bound_molety="Pahk predicted site"
/bound_molety="Pahk predicted site"
/bound_molety="Nagc documented site"
predicted +1 start at 3911406"
                                                                                                                                                                  Sugar-nucleotide biosynthesis, conversions"
/note="f456; ??? pct identical to GLMU_ECOLI SW:
P17114;similar to Bacillus subtilis tms; correction
                                                                                                                     /gene="glmU"
/function="enzyme; Central intermediary metabolism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/product="membrane-bound ATP synthase, Fl sector,
epsilon-subunit"
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beta-subunit"
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anterconversion and pot identical to ATPB_ECOLI alternate gene names uncD, papB; CG Site No.
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/gene="atpC"
/EC_number="3.6.1.34"
/function="enzyme; ATP-proton motive force
                                                                                                                                                                                                                                                                                                    /product="N-acetyl glucosamine-1-phosphate uridyltransferase"
  /note="factor Sigma70; complement(2283. .3653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2463. .2479)
/gene="glmU"
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                                                                                              complement(2283, .3653)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MPELPEVETSRRGIEPHLVGATILHAVVRNGRLRWPVSEEIYRL
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NKLVVGVGNIYASEELFAAGI
NCATOPlement (1. .544)
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                                                                                                                                                                                                                                                                       BCT 07-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli K12 strain MG1655; lambda clones EC14-52, EC17-187, EC27-890, EC21-99, EC22-175, EC27-236, EC17-30, EC17-137, EC15-15, EC17-159; subclones in M13mpl9 or Janus. Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 136254)
Burland, V., Plunkett, G. III, Daniels, D.L. and Blattner, F.R.
DNA sequence and analysis of 136 kilobases of the Escherichia coll
genome: organizational symmetry around the origin of replication
Genomics 16 (3), 551-561 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                  Gaps
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/db_xref="G1:643609"
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                                       Score 22; DB 1; Length 14526;
Pred. No. 3.5;
                                                                                  Indels
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                                                                                                                                                                                                                                                          E. coli; the region from 81.5 to 84.5 minutes. L10328
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/note="X06036; ECOFPG(1..>669)"
1...11607
complement(<1...544)
/gene="fpg"
/note="alternate gene name mutH"
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                                    0.6%; Score 22; DB
llarity 100.0%; Pred. No. 3.5
Conservative 0; Mismatches
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608-263-7459
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1. .136254
                                                                                                                       Laboratory of Genetics
University of Wisconsin
445 Henry Mall
Madison WI 53706
10057. .10059
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                                                          Similarity
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Complement(830..1066)
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/db_xref="G1:290486"
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TLESPEMTRETLGSCTGEEREIFM/IFLDSGIRVITHRRLFSGTLNHYEVHPREIIRE
AIKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDLRVLDHIVIGRGEYVSF
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complement(1283..1957)
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/note="differs from radc sequence in X63366; similar to aureus putative 25 kb protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1168..1819)
//note="x6336; ExcRabC(1..651)"
complement(1212..1240)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1911. .1940)
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complement(557. .586)
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                                                                                                                                                                                                                                                                            618. .623
/note="TTTTTT in X06036; TTTTT in J01677 and here"
                                                                                                                                                    /note="AAAAA in X06036; AAAAAA in J01677 and here"
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/note="promoter-like sequence; promoter matrix
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                                                                                                                                                                                                                                                        and here"
                                                                                                                                                                                                   /note="G in J01677; A in X06036 and here"
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                                                                                                                                                                                                                             /note="G in J01677; A in X06036
misc_difference 618. .623
                                                                                                                                                                                                                                                                                                                              complement(642. .809)
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complement(642. .809)
                                                                                                                                                                                                                                                                                                                                                             /gene-"rpmG (CG Site No. 236)" /rodon_start-1
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/note="T in J01677; TAT here"
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1 (sites)
Makino, K., Yokoyama, K., Kubota, Y., Yutsudo, C.H., Kimura, S.,
Kurokawa, K., Ishli, K., Hattorl, M., Tatsuno, I., Abe, H., Ilda, T.,
Yamamoto, K., Ohnishi, M., Hayashi, T., Yasunaga, T., Honda, T.,
Sasakawa, C. and Shinagawa, H.
Complete nucleotide sequence of the prophage VT2-Sakai carrying the
verotoxin 2 genes of the enterohemorrhagic Escherichia coli O157:H7
Genes Genet. Syst. 74 (5), 227-239 (1999)
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Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Linformation Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mall:Rengen-info.Osaka-u.ac.jp,
URL:http://www.gen-info.Osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                              AP002566 280900 bp DNA linear BCT 07-MAR-2001
Escherichia coli 0157:H7 DNA, complete genome, section 17/20.
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
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Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
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Yokoyama, K., Makino, K., Kubota, Y., Watanabe, M., Kimura, S.,
Yuksudo, C.H., Kurokawa, K., Ishii, K., Hattori, M., Abe, H., Iida, T.,
Yanamoto, K., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C.
                                                                                                                                                                                                                                                                                                                                                                                                           DNA.
szeherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinagawa,H.
Complete nucleotide sequence of the prophage VTI-Sakal carryin Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakal outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Escherichia col1 0157:H7'
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VAGVAALKDHRRYVOFFAFINNVEETARQKRIKKNEDLICANDVSQPTQGFNSDNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"23 kD protein"
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4489. 4514
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Pred. No. 3.5;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2982. 4591

/octe-"X01714; ECOPYREA(1. .1609)"

2982. 5552

/note-"Y01578; ECODUTPYR(1. .2568)"

3324. 3779

/gene-"dut (CG Site No. 832)"

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100.0%; Pre
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                                                                                                                                                                             /codon_start=1
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/gene="ttk"
3844. ,4482
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Matches
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2452 atttatatcgttgtcggtcaac 2473

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CDS

gene

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FLVARFTORVANTAASQRYLEKHPLSRPDELEHHSCILIDSMHIDDANIWRFNVAGS
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ELPERITDSSMIDDRNESFIFVTGVSWRF"
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SCASIGLMMFARMLEWEGDSQYADVWERALYYNTJGGWALDGKHFFYVNPLEVHPKS
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GRSLHMLWLDPADPFTTFEGGETESHKILLGARGYRYGGSPRYNYGHYRNYGRYAIQRGPLYYCLEKADN
TQTLTFIPWFSWANRGEGEMRIWVDERHCHP*
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ERDIDVARONYLAQERSVASSAAEQKQIQSQLDSLVLGEHSQIASLKAQLAEAKYNLE
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                                                                                                                                                                                                                                      complement(5412. .6152)
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complement(5412. .6152)
/gene="ECS44614"
/note="similar to YIAT_ECOLI gi|1790010 percent identity
99 in 246 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to YIAV_ECOLI gi|1790012 percent identity 99 in 378 aa, similar to YIBH_ECOLI gi|1790024 percent identity 76 in 378 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to YIAU_ECOLI gi|1790011 percent identity 99 in 324 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 3.5;
Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6276. .7250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ECs4461"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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22; Conserv
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MMPOLE22
LOCUS
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1901. 3301
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FLIFFYTDVFGLTPALVGTLETALRYPDAISDPWGYIADRROSRWGRFRPWGLWIA
FOLTIGLITTYVPDASWGYKIAWAFGYLLLSVGTAINVPYCARINTWITRHNEVIS
COSWREYLCCYAGFLYVSVGLFWMYALFGOGGNARGYQLGGVGYLCAINVWHFLCTFFWY
RERVPLSTWGKFTLREHLAGLRNNDQLLLMLVWSFLLINVFNIRGGGYMFFITYVLQG
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YQTLMLAVILGNGYLIGGSVLYSPLTRRFDTWKIYYTNILLAALAVLWIMFLPSGPA
ASSAGIISLLEFFWATQCQFGRENQTASSLGGGTAAMFTLRAGAINFFTKLAW
MMSRIATDLRQRHVQP**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MNISEVDLHKLTVSDPFLGGYQQLVRDVVIPYQWDALNDRIPEA
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                                                         /note="similar to XIAI_ECOLI YIAI_ECOLI gi\2367245 percent identity 98 in 157 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notew"unknown,similar to hypothetical protein [Thermotoga
maritima] gi|7452109|pir||F72395 percent identity 37 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1901. .3301
/gene="Ecs458"
/note="probable permease, similar to hypothetical proteins forte="probable permease, similar to hypothetical proteins [Salmonella typhimurium] gi17442781/piri/[C65167] percent identity 37 in 444 aa, also similar to transport proteins (putative symporters) e.g. YicJ [Escherichia coli (K-12)] /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"probable transcriptional regulator weakly similar to hypothetical transcriptional regulator Yisk [Bacillus subtilis] gi[3123306]sp[P40331 percent identity 24 in 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence-not_experimental
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AF12638 1.1294 .416,AF126399.1127 .426,
AF126399.1163 .1216,
AF126390.1163 .1242,AF126390.11469 .622,
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AF126397.1130 .255,133 .222,307 .420)
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307. .630
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                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 824)
Huang, D., Knuuti, R., Palosaari, H., Pospiech, H. and Syvaoja, J.E. CDNA and structural organization of the gene Polel for the mouse Blochim. Blophys. Acta 1445 (3), 363-371 (1999)
                   Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 48 and 49 and complete cds.
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2 (bases 1 to 824)
Huang, D., Knuuti, R., Palosaari, H., Pospiech, H. and Syvaoja, J.
Direct Submission
Submitted (OB-FEB-1999) Department of Biochemistry, University
Oulu, Linnanmaa, Oulu 90570, Finland
Location/Qualifiers
                                                                        AF126398
AF126398.1 GI:5669842
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Mus musculus
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/organism="Mus musculus"
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/clone="MGC:7677 IMAGE:3496540"
/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
                                       Mus musculus, Similar to DNA polymerase epsilon, clone MGC:7677 IMAGE:3496540, mRNA, complete cds.
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TLIRTEVFMEQIRIEQNIAKYYSMSYLQETIEMLLQTSPVSNC"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs refmail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943

Web site: http://www.shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 8 Row: h Column: 8 This clone was selected for till length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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100.0%; Pred. No. 13;
.ive 0; Mismatches 0; Indels
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196. ,1158
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RESULT

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Huang, H. and Brown, D.D.
Prolactin is not a juvenile hormone in Xenopus laevis metamorphosis
Proc. Natl. Acad. Sci. U.S.A. 97 (1), 195-199 (2000)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipldae;
Xenopodinae; Xenopus.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Huang, H. and Brown, D.D.
Direct Submission
Submitted (12-0CT-1999) Embryology, Carnegie Institution of
Washington, 115 W. University Parkway, Baltimore, MD 21210, USA
Location/Qualifiers
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Dev. Growth Differ. 42 (2), 167-174 (2000)
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prolactin receptor.
Xenopus laevis tissue_lib:kidney cDNA to mRNA.
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/protein_id-"AAF05776.1"
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Skatrud, P.Luther, de Waard, M.A., Andrade, A.C. and Peery, R. Brown.
Multiple drug resistance gene atrD of Aspergillus nidulans
Patent: US 6228615-A 1 08-MAY-2001;
                                       Direct Submission
Submitted (27-JUL-1999) Takashi Yamamoto, Faculty of
Science, Kumamoto University, Department of Biological Science;
Kurokami 2-39-1, Kumamoto, Kumamoto 860-8555, Japan
(E-mall:tybig@po.kumamoto-u.ac.jp, Tel:81-96-342-3430(ex.3430),
Fax:81-96-342-3431)
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208. 2043
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Sequence 1 from patent US 6228615.
AR149776.1 GI:15114367
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RESULT 14

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Nascimento, A.M., Terenzi, M.F., Goldman, M.H.S. and Goldman, G.H.
Nascimento, A.M., Terenzi, M.F., Goldman, M.H.S. and Goldman, G.H.
Aspergillus nidulans
Unpublished
2 (bases 1 to 4569)
Nascimento, A.M., Terenzi, M.F., Goldman, M.H.S. and Goldman, G.H.
Direct Submission
Submitted (29-JUL-1999) Ciencias Farmaceuticas, FCFRP-Universidade
de Sao Paulo, Av. do Cafe S/N, Ribeirao Preto, SP 14040-903, Brazil
Location/Qualifiers
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   PAT 08-AUG-2001
                                                                                                                                  Unclassified.
Unclassified.
1 (bases 1 to 4002)
1 (bases 1 to 4002)
Satrud, P.Luther, de Waard, M.A., Andrade, A.C. and Peery, R. Brown.
Multiple drug resistance gene atrD of Aspergillus nidulans
Patent: US 6228615-A 3 08-MAY-2001;
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Emericella nidulans
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Eukaryota; Vangl. Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 4569)
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join(41. 405,457 .3740,3798. .>
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches
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Sequence 3 from patent US 6228615.
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EGGTHSELVQRKGRYYELVNUQSLGKGH"
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1101 BASE COUNT ORIGIN

ó Gaps ö Query Match

0.6%; Score 21; DB 8; Length 4569;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels

Ay 3553 gaagcgacgtcagcctcgac 3573 by 3913 gaagcgacgtcagccctcgac 3573 bb 3913 gaagcgacgtcagccctcgac 3933

Search completed: April 27, 2002, 05:55:01 Job time: 18538 sec

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